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Aaw89251 Mouse PTP
Aaw89250 Mouse PTP
Aaw89263 Human PTP
Aaw89263 Human PTP
Aaw89265 Human PTP
Aaw89265 Human PTP
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Aaw8925 Rat Human Kin
Aae37994 Human Kin
Aae1796 Human Kin
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Compugen Ltd.
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GenCore version (c) 1993 - 2004
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    protein search, using sw model

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AAB59389	AAG78287	AAR60877	AAB56372	AAY81783	AAY56098	AAM23746	AAU14379	AAR75201	ABB57380	ADE57115	ADE57119	ADD47013	ADD47017	AAR72858	AAE37971	ADD46989	AAY81785	AAY56100	AAB19712	
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56	27	28	29	30	31	32	33	34	32	9	37	38	6.6	40	41	42	4.3	44	45	

ALIGNMENTS

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New nucleic acid encoding specific protein tyrosine phosphatases - useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease.
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                                                                                                                                                                                                                   PTP04; FTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease;
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AAW89249 standard; protein; 426 AA.
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, Hui TH;
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Courtneidge SA, App H,
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N-PSDB; AAV81744.
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substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor particularly for treating Alzhedimer's, Parkinson's or Huntington's particularly for treating Alzhedimer's, Parkinson's or Huntington's proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA, to generate transgenic animals and in generate appropriationally after mutation). Ab are used to determine the
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Sequence 426 AA;

240 SFSDKYELVYPEPLESDTDETVWDVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSK 120 SFSDKYBLVYPRPLESDTDETVWDVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSK 120 DIETSVSEKELTQLAQIRPLIFNSSARSAMRDCLNTLQKKEELDIIRRFLELEQMTLPDD 180 181 FNSGNTLQNRDKONRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEERYPYIATQGPLPE 240 TIEDFWOMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHPSVFLETFHVTQY 300 FIVRVPQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCS 360 FIVRVFQIVKKSTGKSQCVKHLQPTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCS 360 9 1 MSSPRKVRGKTGRDNDEEEGNSGNIMLRNSLPSSSQKMTPTKPIFGNKMNSENVKPSHHL 60 1 MSSPRKVRGKFGRDNDEBBGNSGNINLRNSLPSSSQKWTPTKPIFGNKWNSBAVKPSHHI FNSGNTLQNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYPYIATQGPLPE 0; Gaps 100.0%; Score 426; DB 2; Length 426; 100.0%; Pred. No. 0; 0; Indels 0; Mismatches Local Simitarity hes 426; Conservative NLLALY 426 NLLALY 426 61 241 Query Match 121 181 301 301 421 421 Best Loca Matches Ω κ Ω Ω > Ω Ω

AAW89251 standard, protein, 405 AA. 10-MAR-1999 (first entry) Mouse PTP05 isoform #2. ESULT 2 ANUNERBREKSKERA

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PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease, Huntington's disease.

Wus sp

WO9849317-A2

05-NOV-1998

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The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTPD5, PTP10, ALP and ALK-7 proteins. The present sequence represents mouse PTP05. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTP8) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and proteins, particularly cancer (e.g. leukaemia and serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polymucleotides encoding the proteins can be used as probes to identify and clone related sequences; to defect protein-encoded RNA; to generate transgenic animals and in gene the property of the public acid fragmention). Ab are used to determine the
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                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding specific protein tyrosine phosphatases - v for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease.
                                                                                                                                                                                                                        Jallal B, Peles E, Omrust S, Markby D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.1%; Score 405; DB 2; Length 405;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 158-160; 193pp; English.
                                                                                                                                                                                                                                          Courtneidge SA, App H, Hui TH;
                                                         97US-0047222P.
97US-0049477P.
97US-0049756P.
97US-0049914P.
97US-0063595P.
  98WO-US008439,
                                       97US-0044428P
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405; Conservative
                                                                                                                                                                                                                        Clary D,
                                                                                                                                                                                                                                                                                   WPI; 1999-009434/01.
                                                                                                                                                                                (SUGE-) SUGEN INC.
                                                                                                                                                                                                                                                                                                       N-PSDB; AAV81746.
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27-APR-1998;
                                                                                                                                                                                                                        Plowman GD,
                                                                                                                                           23-0CT-1997;
                                                                                                     1-JUN-1997
                                                                               .1-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful
                                                                                                                                                                                                        type i receptor serine/threonine kinase; cancer; leukaemia; lymphoma;
neurodegenerative disease; neuronal survival; Alzheimer's disease;
Parkinson's disease; Huntington's disease.
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                                                                                                                                                                                    SAD; ALP; ALK-7; protein tyrosine phosphatase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding specific protein tyrosine phosphatases for identifying specific modulators for treatment and prevention cancer and neurodegenerative disease.
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100.0%; Pred. No. v.
... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  allal B,
Hui TH;
    AAW89250 standard; protein; 463
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97US-0049477P.
97US-0049756P.
97US-0049914P.
97US-0063595P.
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                                                                                          (first entry)
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Courtneidge SA, App
                                                                                                                                                                                       PTP04; PTP05; PTP10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-009434/01.
N-PSDB; AAV81745.
                                                                                                                                        Mouse PTP05 isoform
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18-JUN-1997;
23-OCT-1997;
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Best Local Simi
Matches 383;
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                                                                                          10-MAR-1999
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The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These
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                 284 EFEHFSVFLETFHVTQYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYV
                                                                                                                                                                                           321 BFEHFSVPLRFFPHVTQYFTVRVFQIVKKSTGKSQCVKHLQPTXWPDHGTPASADPFIKYV
                                                                                                                                                                                                                                        164 DIIREELEQMTLPDDFNSGNTLQNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTP04, PTP05, PTP10, SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease;
                                                                            224 NHEREYFYIATQGPLPETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPL
                                                                                                                                   161 NHEEBYFYIAIQGPLPETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPL
                                                                                                                                                                                                                            344 RYVRKSHITGPLLVHCSAGVGRIGVFICVDVVPSAIEKNYSFDIMNIVTQMRKQRCGMIQ
104 PSKTVSPVLSGSSRLSKOTBTSVSEKELTQLAQIRPLIFNSSARSAMRDCLNTLQKKEEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding specific protein tyrosine phosphatases - 1 for identifying specific modulators for treatment and prevention of
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Hui TH;
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970S-0049477P.
970S-0049756P.
970S-0049914P.
970S-0063595P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human PTP05 peptide 431A.
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Courtneidge SA, App H,
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cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polymucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the proteins. The present sequence represents a human PTPOS peptide from the present invention

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Gaps

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Indels

6.8%; Score 29; DB 2; Length 29; 100.0%; Pred. No. 1.3e-21;

Sequence 29 AA;

Query Match

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substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzhaimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polymucleoties encoding the proteins can be used as probes to identify and clone related and in gene therapy (optionally after mutation). Ab are used to determine the proteins. The present sequence represents a human PTP05 peptide from
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                                                                                                                                                                                                                                                                                                                                                                                                                                   109 SPVISGSSRISKDTETSVSEKELTQLAQI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPALSGSSRLSKDTETSVSBKELTQLAQI 29
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Courtneidge SA, App H, Hui TH;
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97US-0047222P.
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                                                                                                                                                                                                                                                                                                                                                                                        29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PTP05 peptide 433A.
                                                                                                                                                                                                                                            present invention
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Best Local Similarity
Matches 29; Conserv
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                                                                                                                                                                                                                                                                                               Sequence 29 AA;
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20-MAY-1997;
11-JUN-1997;
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The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The above proteins, other than ALK-7, are protein tyrosine phosphates. The above proteins, other than ALK-7, are protein tyrosine phosphates the acivity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphomal), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful
                                                                                                                                                                                                                                                                 PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding specific protein tyrosine phosphatases for identifying specific modulators for treatment and prevention cancer and neurodegenerative disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peles E,
Local Similarity 100.0%; Pred. No. 1.3
                                               23
                                            1 MSSPRKVRGKTGRDNDBEEGNSGNLNLRN
                                                                 1 MSSPRKVRGKTGRDNDEEEGNSGNLNLRN
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Hui TH;
                                                                                                                                                   AAW89265 standard; peptide; 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0044428P.
97US-0047222P.
97US-0049477P.
97US-0049756P.
97US-0043595P.
                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-US008439
                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                          Human PTP05 peptide 432A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plowman GD, Clary D, J
Courtneidge SA, App H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-009434/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SUGE-) SUGEN INC.
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                             WO9849317-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                      27-APR-1998;
                                                                                                                                                                                                              10-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                         05-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-1997
                                                                                                                                                                                 AAW89265;
                    Matches
                                                                                                                                          AAW8926
                                                                                                                          RESULT
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The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly

Example 14; Page 108; 193pp; English.

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survival, particularly for treating Alzheimer's, Parkinson's or function's diseases. Nucleic acid fragments of the polyuacleorides encoding the proteins can be used as probes to identify and clone related sequences, to detect protein-encoded RNA, to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the proteins. The present sequence represents a human PTPOS peptide from the present invention
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Sequence 29 AA;

Gaps ö Length 29; 0; Indels 6.8%; Score 29; DB 2; Le 100.0%; Pred. No. 1.3e-21; live 0; Mismatches 0; 83 WDVSDRSLRNRWNSMDSETAGPSKTVSPV 111 Conservative Similarity 29; Query Match Local Best Loca Matches

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WDVSDRSLRNRWNSMDSETAGPSKTVSPV 29

1W89252

AAW89252 standard, protein, 122

AAW89252;

entry) (first 10-MAR-1999

type i receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease; Huntington's disease. PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; tyrosine phosphatase; receptor serine/threonine kinase: cancer: lankaomia. lymnhym

Rattus sp.

W09849317-A2

98WO-US008439 27-APR-1998;

97US-00472222P. 97US-0049477P. 97US-0049756P. 97US-0049914P. 97US-0063595P. 97US-0044428P 20-MAY-1997; 28-APR-1997 11-JUN-1997 18-JUN-1997 11-JUN-1997

(SUGE-) SUCEN INC.

23-OCT-1997;

Markby D; Ś Onrust Peles E, πE Jallal , Hui T ï Ď App Clary Courtneidge SA, 9 Plowman

WPI; 1999-009434/01. N-PSDB; AAV81747.

당 New nucleic acid encoding specific protein tyrosine phosphatases for identifying specific modulators for treatment and prevention cancer and neurodegenerative disease.

Claim 2; Page 160; 193pp; English.

The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALD and ALK-7 proteins. The present sequence represents rat PTP10. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify substances that modulate their activity (i.e. agonists and ansagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leuksemia and lymphoma), while modulators of ALK-1 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival,

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particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleocides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the
                                                                                                                                                                                                                                                                                                                                                                                                                            Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis; atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer; psoriasis; thrombocytopaenia; developmental disorder; Reiter's syndrome; renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease; neurological disorder; parkinson's disease; epilepsy; glomerulonephritis; autoimmune disorder; planmatory disorder; AIDS; Goodpasture's syndrome; acquired immune deficiency syndrome; immunosuppressive; Crohn's disease; noctropic; transgenic; dermatitis; multiple sclerosis; diabetes mellitus; allergy; gout; Grave's disease; mashimotopic; the syndrome; osteoporosis; rheumatorid arthritis; Sjogren's syndrome; osteoporosis; rheumatorid arthritis; Sjogren's syndrome; ophthalmological; gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.
                                                                                                                                                                    Gaps
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0
                                                                                                                                   5.4%; Score 23; DB 2; Length 122;
100.0%; Pred. No. 6.8e-15;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Human kinase and phosphatase (KPP-39) protein.
                                                                                                                                                                                                   DFFIKYVRYVRKSHITGPLLVHC 359
                                                                                                                                                                                                                       DFFIKYVRYVRKSHITGPLLVHC 116
                                                                                                                                                                                                                                                                                                             Ä
                                                                                                                                                                                                                                                                                                             AAE37994 standard; protein; 261
                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                    23; Conservative
                                                                                                                                                       Similarity
                                                                                                           Sequence 122 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                        06-NOV-2003
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                                                                                                                                       Query Match
Best Local
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                                                                                                                                                                                                                                                                              RESULT 8
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Marquis JP; Gorvad AE; Griffin JA, Marquis R, Lee S, Hawkins PR; Chien D, Wilson AD, Swarnakar A, Go A, Baerling BM, Ramkunar J, Jin P, ' Chawla NK, Lehr-Mason PM, Khare R, Lee SY, Sprague WW, Zebarjadian Y; (INCY-) INCYTE GENOMICS INC. Lee SY, AJA, Baughn MR, Becha SD, Kable AE, Hafalia

19-DEC-2001; 2001US-0343007P. 21-DEC-2001; 2001US-0343546P. 04-FEB-2002; 2002US-035438BP. 15-FEB-2002; 2002US-0357675P.

06-DEC-2002; 2002WO-US039126 07-DEC-2001; 2001US-0340235P

WO2003050084-A2.

WPI; 2003-532894/50. N-PSDB; AAD57366 New human kinases and phosphatases and polymucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. ADE), allergy or anemia), multiple sclerosis, osteoarthritis, cancer or hepatitis.

Claim 1; Page 242; 282pp; English

The invention relates to an isolated polypeptide, which is a human kinase and phosphatase (KPP). KPP agonists and antagonists are useful for

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diagnosing, treating or preventing disorders associated with aberrant expression of RPP, particularly cell proliferative disorders (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary thromobocytopaenia or cancer), developmental disorders (e.g. renal tubular acidosis, anaemia or mental retardation), neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/inflammatory disorders (e.g. AIDS; acquired immune deficiency syndrome, allergies, asthma, autoimmune thyroiditis, contact dermattisis, Crohn's disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, qout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome, multiple scherosis, osteoarchritis, osteoarchritis, osteoarchritis, osteoarchritis, osteoarchritis, osteoarchritis, vorse of exceptonosis, pancreatiis, Reler's syndrome, uveitis), osteoarchritis, Syogren's syndrome, uveitis), or viral, bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP is useful in assessing the effects of exceptones compounds on the expression of nucleic acids and kinases and phosphatases. KPP gene is useful in gene therapy and for creating transgenic animals to model human disease. The present sequence is human KPP protein

Sequence 261 AA;

Gapa ö 4.5%; Score 19; DB 6; Length 261; 100.0%; Pred. No. 1.7e-10; 0; Indels 100.0%; Prec. nc. Conservative Query Match Best Local Similarity 1

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192 KARYRDILPYDSTRVPLGK 210

27

3G30845 SULT

ABG30845;

ABG30845 standard; protein; 398 AA.

(first entry)

21-0CT-2002

Human tyrosine phosphatase protein #1.

Human, tyrosine phosphatase; obesity, diabetes; Parkinson's disease; central nervous system disorder; CNS; cardiovascular disorder; stroke; chronic obstructive pulmonary disease; cancer; multiple sclerosis; Alzheimer's disease; Huntington's disease; congestive heart failure; myocardial infarction; chromosome 10.

Homo sapiens

WO200242435-A2.

30-MAY-2002.

27-NOV-2001; 2001WO-EP013794

27-NOV-2000; 2000US-0252912P

(FARB) BAYER AG

Zhu Z;

WPI; 2002-575236/61. N-PSDB; ABK89178.

New human tyrosine phosphatase polypeptide, the regulation of which is useful for treating obesity, diabetes, cardiovascular or central nervous system disorder, chronic obstructive pulmonary disease and cancer.

Claim 25; Fig 2; 145pp; English.

The present invention relates to a new human tyrosine phosphatase polypeptide. The invention is useful for the preparation of a medicament for modulating the activity of human tyrosine phosphatase in a disease such as obesity, diabetes, a central nervous system (CNS) disorder,

ö chronic obstructive pulmonary disease, cardiovascular disorder or cancer. The invention is useful for treating a human tyrosine phosphatase dysfunction related disease, preferably the above mentioned diseases. The invention is useful for treating the above mentioned diseases. The trovention is useful for treating the above mentioned disorders, where the CNS disorder is selected from Parkinson's disease, multiple sclerosis, stroke, Althelmer's disease, and Huntington's disease, multiple sclerosis, adjagnostic assays for detecting from congestive heart failure and myocardial infarction. The molecules of the invention are useful in susceptibility to disease and abnormalities related to the presence of susceptibility to disease and abnormalities related to the presence of mutations in the polymucleotide coding the polypeptide of the invention. The present amino acid sequence represents the human tyrosine phosphatase protein #1 of the invention. This sequence is encoded by the human tyrosine phosphatase tyrosine phosphatase discount and processes and abnormality to the human tyrosine phosphatase tyrosine phosphatase gene located on chromosome 10 The present invention describes an isolated cancer associated phosphatase nucleic acid. Also described: (1) a method of screening for biologically active agents that modulate a cancer associated phosphatase function; (2) a method for the diagnosis of cancer; (3) a method for inhibiting the growth of a cancer cell; (4) methods of screening for targets of a cancer cancer associated phosphatase; enzyme; human; cancer; tumour; cytostatic; immunosuppressive; antidiabetic; neuroprotective; antirheumatic; antisathritic; antissoriatic; antiarterioscalerotic; antiantammatory; vulnerary; gynaecological; antiantogenic; hyperproliferative disease; autoimmune disease; diabetes mellitus; multiple sclerosis; rheumatoid arthritis; pseriasis; atherosclerosis; inflammation; scarring; 벙 New nucleic acids encoding cancer associated phosphatases, useful as targets for screening pharmaceutical agents that inhibit the growth ctumor cells, or for diagnosing and treating cancer, inflammation or ö Length 398; Indels 4.5%; Score 19; DB 5; Le 100.0%; Pred. No. 2.6 tive 0; Mismatches Human DKFZP566K0524 protein SEQ ID NO:10. Claim 1; SEQ ID NO 10; 63pp; English. ADD89795 standard; protein; 398 AA. 192 KWRYRDILPYDSTRVPLGK 210 164 KNRYRDILPYDSTRVPLGK 182 28-MAR-2002; 2002US-0368859P. 19-MAR-2003; 2003WO-CA000393 endometriosis; angiogenesis. (first entry) (KINE-) KINETEK PHARM INC. 19; Conservative WPI; 2003-902934/82. N-PSDB; ADD89794. autoimmune disease. Local Similarity Sequence 398 AA; WO2003083102-A2. 29-JAN-2004 09-OCT-2003. Delaney AD; ADD89795; Query Match Matches RESULT 10 ADD89795 કે 셤

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associated phosphatase, where the targets are associated with signal transduction in cancer cells; (5) a compound (C) for the treatment of a tumour; (6) a composition a pharmaceutical carrier and (C); (7) methods for treating a tumour; and (B) a method for visualising a tumour in a patient. A cancer associated phosphatase of the present invention has cytostatic, immunosuppressive, antidabetic neuroprotective, antirheumatic, antiarthritic, antiateriosclerotic, antinheumatory, vulnerary, antipsoriatic, antiarteriosclerotic, antinhelmmatory, vulnerary, antipsoriatic antiarteriosclerotic, antinhelmmatory, vulnerary, antipsoriatic antiarteriosclerotic, antiarthritic, antiarteriosclerotic, antiarthritic, synaecological and antianquogenic activities. The cancer associated phosphatases and nucleic acids encoding the proteins are useful for visualising tumours in patients or chalon cancer. The polypeptides and nucleic acids may also be used for treating hyperproliferative diseases, such as autoimmune disease, diabetes mellitus, multiple sclerosis, rheumatoid arthritis, psoriasis, atherosclerosis, inflammation, scarring, endoametriosis or angiogenesis, determining the effectiveness of drugs, determining patient prognosis, or as targets for screening pharmaceutical agents that inhibit the growth or metastasis of tumour cells. The present sequence represents the human cancer associated phosphatase

ENERGESCSCS, which is used in the exemplification of the present invention.
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Sequence 398 AA;

Query Match
4.5%; Score 19; DB 7; Length 398;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps
, 192 KARYRDLLPYDSTRVPLGK 210

ö

192 KNKIKDILPIDSIKVPLGK ZIC

164 KARYRDILPYDSTRVPLGK 182

ISULT 11)E09123) ADE09123 standard; protein; 409 AA.

ADE09123;

(first entry)

29-JAN-2004

Novel protein-related contig polypeptide sequence #189

novel gene; novel protein; tissue marker; molecular weight marker; chromosome marker; genetic disorder; contig.

Unidentified.

WO2003054152-A2.

03-JUL-2003.

10-DEC-2002; 2002WO-US039555

10-DEC-2001; 2001US-0339739P-11-DEC-2001; 2001US-0339453P-14-MAR-2002; 2002US-0365091P-

14 MAR-2002, 2002US-0365384P. 12-APR-2002, 2002US-0372381P. 12-APR-2002, 2002US-037281SP. 22-APR-2002, 2002US-03128558. 24-APR-2002, 2002US-0376045P.

(HYSE-) HYSEQ INC.

Tang YI, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J; Ghosh M, Xue AJ, Wehrman I, Weng G, Zhou P, Drmanac RI, Wang Z; Ma Y, Wang D, Chen R, Xu C, Boyle BJ;

WPI; 2003-569235/53.

New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues

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Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis; atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer; psoriasis; thromobocytopaenia; developmental disorder; Reiter's syndrome; renal tubular acidosis; anaemia; mental retadation; Alzheimer's disease; neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis; autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome; aquired immune deficiency syndrome; immunosuppressive; croun's disease; noctropic; transgenic; dermatitis; multiple solerosis; diabetes mellitus; allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome; osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological;
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, Griffin JA, Marquis JP;
R, Lee S, Hawkins PR;
                                                                    The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
                                                                                                                                                                                                                                                                                                                    Gaps
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in which the corresponding protein is preferentially expressed
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                                                                                                                                                                                                                                                                                Length 409;
                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chien D, Wilson AD, Swarnakar A, Go
A, Bmerling BM, Ramkunar J, Jin P, '
Chawla NK, Lehr-Mason PM, Khare R,
Lee SY, Sprague WW, Zebarjadian Y;
                                                                                                                                                                                                                                                                            4.5%; Score 19; DB 7; L6
100.0%; Pred, No. 2.6e-10;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human kinase and phosphatase (KPP-41) protein.
                                      Disclosure; SEQ ID NO 2667; 1177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE37996 standard; protein; 412 AA.
                                                                                                                                                                                                                                                                                                                                                          KNRYRDILPYDSTRVPLGK 210
                                                                                                                                                                                                                                                                                                                                                                              19-DEC-2001; 2011US-0343007P.
21-DEC-2001; 2001US-0343546P.
04-FEB-2002; 2002US-0354388P.
15-FEB-2002; 2002US-0357675P.
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                                                                                                                                                                                                                                                                                                  Local Similarity 100.
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                                                                                                                                                                                                                                              Sequence 409 AA;
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Baughn MR,
                                                                                                                                                                                                                                                                                                                                                          192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE37996;
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                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
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  #X8X88888888888888888
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The invention relates to an isolated polypeptide, which is a human kinase and phosphatase (KPP). KPP agonists and antagonists are useful for diagnosing, treating or preventing disorders associated with aberrant expression of KPP, particularly cell profiferative disorders (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal nocturnal heemoglobinuria, polycythaemia vera, psoriasis, primary thromobocytopaemia or cancer), developmental disorders (e.g. acidosis, anaemia or mental retardation), neurological disorders (e.g. Alrahemer's disease, parkinson's disease or epilepsy), autoimmune, inflammatory disorders (e.g. Alibs, acquired immune deficiency syndrome, allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome, multiple sclerosis, osteoarthritis, steporosis, pancreatitis, Reiter's syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral, bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP is useful in assessing the effects of exogenous compounds on the expression of nucleic acids and kinases and phosphatases. KPP gene is useful in gene therapy and for creating transgenic animals to model human disease. The present sequence is human KPP protein
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/mote= "Tyrosine specific protein phosphatase active
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100.0%; Pred. No. 2.6e-10;
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/note= "Protein-tyrosine phosphatase"
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/note="Tyr_phosphatase"
362..379
/label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. No 2.6
:ive 0; Mismatches
                                                            Claim 1; Page 243-244; 282pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein phosphatase-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19; Conservative
cancer or hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 412 AA;
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22-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-2002
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Matches
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The present sequence is human protein phosphatase (PP)-4. PP

CC polyuclectide and polypeptide are useful in the diagnosis, treatment and polyuclectide and polypeptide are useful in the diagnosis, treatment and polyuclectide immune system disorders. Examples of developmental disorders and cell proliferative disorders. Examples of immune system disorders include acquired immune deficiency syndrome (AIDS), adult treatment combined immunodeficiency disease (SCID), adult treatment of disease, atopic dermatitis, diabetes mellitus, ceptoacters, crophysema, Goodpasture's syndrome, gout, Graves disease, multiple corporosis, myosathenia gravis myosatial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome, crhematodia trhritis, Sjogren's syndrome, sclaroderma, systemic sclarosis, trauma; neurological disorders include Alzheimer's disease, Huntington's disease, dementia, epilepsy, Parkinson's disease, mental corporation and other developmental disorders of central nervous system cuch as Down's syndrome, cerebral palsy, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders, seasonal caffective disorders include e.g. renal tubular acidosis, Duchenne or developmental disorders include e.g. renal tubular acidosis, Duchenne or developmental disorders include e.g. renal tubular acidosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepaticis, psoriasis and cancer including adenocarcinoma, leukaemia. The polypeptide and polymuclectide are further useful for analysing proteome of a tissue or acell type or its modulator. The polymuclectide is useful for creating knockin the mumanised animals (pigs) or transgenic celling animals (pigs) or transgenic celling animals (pigs) or transgenic celling elementation animals of or each or celling elementation animals of or each or celling animals for celling animals of central or celling animals for celling animals or cell
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                                                                                                                                                            Au-Young J, Baughn MR, Ding L, Elliott VS, Gandhi AR, Griffin JA;
Hafalia A, Kearney L, Lee EA, Lu Y, Nguyen DB, Patterson C;
Ramkumar J, Reddy R, Sanjanwala MS, Stewart EA, Tang YT, Thornton M;
Tribouley CM, Walia NK, Yang J, Yao MG, Yue H;
                                                                                                                                                                                                                                                                                                                                                                                    cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human disease, for generating a transcript image of a tissue or cell type, which represents the global pattern of gene expression by a particular tissue or cell type
                                                                                                                                                                                                                                                                                                                                                          Novel polypeptide, useful for diagnosing, treating or preventing disorders of growth and development, immune system, neurological proliferation diseases, comprises cancer protein phosphatase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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100.0%; Pred. No. 2.7e-10;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 105-106; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE08106 standard; protein; 508 AA.
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29-JUN-2000; 2000US-0215210P.
06-JUL-2000; 2000US-021529P.
12-JUL-2000; 2000US-0218080P.
21-JUL-2000; 2000US-0220117P.
                                                                                                                      (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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nes 19; Conservative
                                                                                                                                                                                                                                                                                       WPI; 2002-090206/12.
                                                                                                                                                                                                                                                                                                                 N-PSDB; AAD24022.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides.
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ADE08106
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Unidentified

novel

03-JUL-2003

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treation (PCR) primers, to isolated polymotrocine (11) and polypeptide (11) requences. (I) is useful as hybridiation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymotenties are also used in diagnostics as expressed sequence tags for identifying expressed control of the control of control of control of the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated polymucleotide (I) and polypeptide (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID NO 36401; 103pp; English
                                                                                                                                                                                                                                                                                                             Tang YT;
                                                                     30-MAR-2001; 2001WO-US008631.
                                                                                                                                    31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
                                                                                                                                                                                                                                                                                                          Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-639362/73
                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS70229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 561 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biodiversity.
11-OCT-2001
   New polynuclectides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed, as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Wang J;
Wang Z;
                                    novel gene; novel protein; tissue marker; molecular weight marker;
chromosome marker; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID NO 1172; 1177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             10-DEC-2001; 2001US-0339739P.
11-DEC-2001; 2001US-0339453P.
14-WAR-2002; 2002US-036593P.
14-WAR-2002; 2002US-0365384P.
12-ARR-2002; 2002US-037281P.
12-ARR-2002; 2002US-037281P.
22-ARR-2002; 2002US-0372615P.
                                                                                                                                                                                                                                                                                                                                               10-DEC-2002; 2002WO-US039555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-APR-2002; 2002US-0376045P
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                                    Gaps
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4.5%; Score 19; DB 4; Length 561;
100.0%; Pred. No. 3.5e-10;
tive 0; Mismatches 0; Indels
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                                                                      192 KNRYRDILPYDSTRVPLGK 210
   Query Match
Best Local Similarity 100.0
Matches 19; Conservative
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Job time :
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Length 508;

4.5%; Score 19; DB 7; Length 508 100.0%; Pred. No. 3.2e-10; ive 0; Mismatches 0; Indels

Local Similarity 100. nes 19; Conservative

Best Loca Matches

Query Match

Sequence 508 AA;

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

WO200175067-A2

Homo sapiens

Novel human diagnostic protein #6033.

13-FEB-2002 (first entry)

ABG06042;

ABG06042 standard; protein; 561 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34, Application US/08446345
Patent No. 5831009
GENERAL INFORMATION:
APPLICANT: Ullrich, Axel
APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Karin B.
TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE
ITILE OF INVENTION: HOSPHATASES PTP-D1
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEB: Pennie & Edmonds
STREET: New York
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: N.Y.

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,345
FILING DATE: 22-MAY-1995
CLLASSIPICATION: 435
PILING DATE: 28-MAY-1995
APPLICATION NUMBER: US 08/234,440
FILING DATE: 28-MAY-1995
APPLICATION NUMBER: US 08/234,440
FILING DATE: 28-MAY-1995
APPLICATION NUMBER: 18-MAY-18-MAME: CONIZZI, LAURA A-
REFERENCE/DOCKET NUMBER: 30742
US-08-685-992-5
US-08-184-925-5
US-08-844-533-2
US-08-015-986A-3
US-08-015-986A-3
US-08-015-986A-3
US-08-015-986A-2
US-08-18-303-2
US-08-31-2
US-08-31-2
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US-08-31-5
US-08-015-985-5
US-08-015-985-5
US-08-015-985-5
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US-08-015-985-7
US-09-280-597-7
US-08-015-985-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 272 amino acids
amino acid
    single
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MOLECULE TYPE: protein
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TOPOLOGY: unknown
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Best Local Similarity
Matches 15; Conserv
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US-08-446-345-34
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    Sequence 34, Appl
Sequence 36, Appl
Sequence 9, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 5, Appli
Sequence 6, Appli
                                                                                                                                                          June 16, 2004, 13:30:21 , Search time 23 Seconds (without alignments) 956.203 Million cell updates/sec
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1 MSSPRKVRGKTGRDNDEEEG......QYQFCYEIVLEVLQNLLALY 426
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Sequence
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1. /cgm2_6/ptodata/2/iaa/5A_COMB.pep:*
2. /cgm2_6/ptodata/2/iaa/5B_COMB.pep:*
3. /cgm2_6/ptodata/2/iaa/6A_COMB.pep:*
4. /cgm2_6/ptodata/2/iaa/6B_COMB.pep:*
5. /cgm2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6. /cgm2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-446-345-36
US-08-449-609-9
US-08-610-96A-9
US-09-361-096A-9
US-09-361-096A-47
US-08-036-210-11
US-08-036-210-11
US-08-036-210-11
US-08-036-11
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US-08-146-13
US-08-146
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US-09-144-925-18
                                                                                                                                                                                                                                                                                                                                                                                                                          389414 segs, 51625971 residues
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                                                                                                                    - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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iximum DB seq length: 200000000
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Match Length
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                                                                                                                                                                                                                                                                                 rfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rd size :
                                                                                                                    f protein
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CORRESPONDENCE ADDRESS:
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100.0%; Pred. No. 4.2e-06;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/08036210
Patent No. 558523
GENERAL INFORMATION:
APPLICANT: Moller, Karin B.
APPLICANT: Moller, Karin B.
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: PHOSPHATASE
NUMBER OF SEQUENCES: 45
                                                                                                                                                          Sequence 36, Application US/08446345
Patent No. 5831009
GENERAL INPORATION:
APPLICANT: Woller, Nael
APPLICANT: Woller, Niels P.H.
APPLICANT: Woller, Nover PROTEIN PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASES PTP-D1
NUMBER OF SEQUENCES:
ADDRESSED: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
GITY: New York
STATE: N.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: N.Y.

COUNTRY: N.Y.

COUNTRY: N.Y.

ZIF: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,345
FILNG DATE: 22-MAY-1995
CLASSIFICATION 1435
FILNG RAPLICATION NUMBER: US 08/234,440
FILING DATE: 28-APR-1994
ATTONENT/AGENTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30742
REFERENCE/DOCKET NUMBER: 7683
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-8864
TELEPAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS:
LENGTH: 1174 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354 PLLVHCSAGVGRTGV 368
                        15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: un
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STREET: 1155 AVENUE & EDWANDS

CITY. New YORK
STATE: New YORK
GONDATE: 1155 AVENUE Of the Americas
CITY: New YORK
GONDATE: 125 AVENUE Of the Americas
CONDATE: 125 AVENUE OF THE AMERICAN OF T
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Two Militia Drive
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                                                                                                ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                    Lexington
                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-685-992-26
                                                                             COUNTRY:
          STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/09361096A
Sequence 9, Application US/09361096A
Patent No. GAPA-103.
APPLICANT: MOLLER, KARIN B.
APPLICANT: MOLLER, KARIN B.
APPLICANT: WILLRICH, AXEL
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE
FILE REFERENCE: 038602/0686
CURRENT APPLICATION NUMBER: US/09/361,096A
CURRENT FILING DATE: 1999-07-26
PRIOR PELING DATE: 1995-07-26
PRIOR PELING DATE: 1995-03-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PACENTIN Ver: 2.1
SEQ ID NO 9
LENGTH: 176
TYPE: PRI
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 176;
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
3.3%; Score 14; DB 2; Length 176
Best Local Similarity 100.0%; Pred. No. 6.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26, Application US/08685992
Patent No. 5912138
GENERAL INFORMATION:
APPLICANT: TORKS, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                           7683-025
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-
TELEPHONE: 212-790-9090
TELEPHONE: 212-790-9090
TELEPAX: 212-968-8884/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 176 amino acids
TYPE: protein
3-08-449-609-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 VHCSAGVGRTGVFI 370
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Best Local Similarity 100.0
Matches 14; Conservative
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S-08-685-992-26
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Matches
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COUNTY: WAS DESCRIBED ONE.

CONTINES: WAS DESCRIBED ONE.

SECTION OF THE RELABBLE FORM: Mindows STEEN, Withholes STEEN, WITHOUT STEEN, WITHOUT STEEN, WITHHOLES STEEN, WITHHOLE STEEN, WITHOUS STEEN, WITHHOLE STEEN, WITHOUS ST
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Patent No. 6492495
GENERAL INFORMATION.
GENERAL INFORMATION.
APPLICANT: WILLER, KARIN B.
APPLICANT: WILLER, KARIN B.
APPLICANT: WILLER, KARIN B.
APPLICANT: WILLER, KARIN B.
TITLE REFERENCE: 038602/0866
CURRENT APPLICATION WUNBER: US/09/361,096A
CURRENT APPLICATION NUNBER: US/09/361,096A
CURRENT APPLICATION NUNBER: 08/449,609
PRIOR PILING DATE: 1995-05-24
PRIOR APPLICATION NUMBER: 08/49,609
PRIOR PILING DATE: 1995-03-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S-08-036-210-11
Sequence 11, Application US/08036210
Pacent No. 528523
Pacent No. 528523
Pacent No. 528523
APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Karin B.
APPLICANT: Ullrich, Arzin B.
APPLICANT: Ullrich, Arzin B.
TITLE OF INVENTION: PHOSPHATASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 289;
                                                                                                                                                                                                                                                                                                                                                                                       Length 245;
                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.3%; Score 14; DB 2; Length 245 Best Local Similarity 100.0%; Pred. No. 9.3e-06; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
3.3%; Score 14; DB 4; Lv
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 14; Conservative 0; Mismatches 0:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL96-03Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
                                                                                                                                             TELEX:
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 VHCSAGVGRTGVFI 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      357 VHCSAGVGRTGVPI 370
                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
3-09-144-925-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -09-361-096A-47
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US-08-449-609-15; Sequence 15, Application US/08449609
1995-03-23
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                                                                                                                                                                                                                                                                                                                                          300 VHCSAGVGRIGVFI 313
PRIOR FILING DATE: 1995-03-2
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 402 amino acida
amino acid
                                                                                                                                                                                                        Query Match 3.3
Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                           US-09-361-096A-15
                                                                                           401
                                                                SEQ ID NO 15
LENGTH: 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INPORMATION: 019-21-21-21
APPLICANT: MOLLER, NIELS P.H.
APPLICANT: MOLLER, XARIN B.
APPLICANT: MOLLER, XARIN B.
APPLICANT: MLAICH, AXEL
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE
FILE REPERENCE: 038602/0686
CURRENT APPLICATION NUMBER: US/09/361,096A
CURRENT FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 08/449,609
PRIOR APPLICATION NUMBER: 08/036,210
PRIOR APPLICATION NUMBER: 08/036,210
PRIOR PILING DATE: 1995-03-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PATENTING DATE: 1955-03-23
TYPE: PATENTING DATE: 2.1
SEQ ID NO 11
LENGTH: 322
TYPE: PRT
TYPE: PRT
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Sequence 15, Application US/09361096A

Patent No. 6492493

GENERAL INFORMATION:

APPLICANT: MOLLER, KARIN B.

APPLICANT: ULLRICH, ARRIN B.

TITLE OF INVENTION: PTP-831: A NOVEL PROTEIN TYROSINE PHOSPHATASE
FILE REPERENCE: 038621/068A

CURRENT APPLICATION NUMBER: US/09/361,096A

CURRENT FILING DATE: 1999-07-26

PRIOR PLING DATE: 1995-05-24

PRIOR PLING DATE: 1995-05-24

PRIOR APPLICATION NUMBER: 08/036,210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.3%; Score 14; DB 4; Length 322; Best Local Similarity 100.0%; Pred. No. 1.2e-05; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                         Score 14; DB 2; Length 322; Pred. No. 1.2e-05; 0; Mismatches 0; Indels
REFERENCE/DOCKET NUMBER: 7683-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :SULT 11
:-09-361-096A-11
Sequence 11, Application US/09361096A
Patent No. 6492495
                                                                                                                                                                                                                                                                                                                            Query Match 3.3%; Soc
Best Local Similarity 100.0%; P.
Matches 14; Conservative 0;
                                                                TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 322 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                       357 VHCSAGVGRTGVFI 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 VHCSAGVGRTGVFI 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                357 VHCSAGVGRTGVFI 370
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                                                                                                                                                                                                     STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                   TOPOLOGY: unknown
MOLECULE TYPE: protein
-08-449-609-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -09-361-096A-15
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Sequence 15, Application US/08036210

Patent No. 556523

PATENT NO. 556523

PAPLICANT: Moller, Niels P.H.

APPLICANT: Moller, Karin B.

APPLICANT: Ullrich, Axel

ITILE OF INVENTION: PTP-831: A NOVEL PROTEIN TYROSINE

ITILE OF INVENTION: PTP-831: A NOVEL PROTEIN TYROSINE

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: RENNIE & EDMONDS

STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
3.3%; Score 14; DB 1; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels
            Length 401;
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNATE: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPATE: BM PC COMPALIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN RELEASE
STATING DATE: 23-MAR-1993
CLASSIFICATION NUMBER: US/08/036,210
FILING DATE: 23-MAR-1993
CLASSIFICATION NUMBER: 18,872
RESERBINGE/DOCKET NUMBER: 7683-025
TELERPATION TOWNER: 7683-025
TELERPATION TOWNER: 12.2-869-864/9741
TELERPATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
               Score 14; DB 4; Le
Pred. No. 1.5e-05;
3.3%; Scc...
100.0%; Pred. No. ...
0; Mismatches
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Patent No. 5586233
GENERAL INFORMATION:
APPLICANT: Moller, Nails P.H.
APPLICANT: Moller, Karin B.
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: PTD-531: A NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSE: PERNIE & EDMONDS
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.3%; Score 14; DB 2; Length 402
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels
                                 APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Karin B.
APPLICANT: Ullrich, Azzin B.
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                     CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-271
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPATION TO PATA:
APPLICATION NUMBER: US/08/449,609
FILING DATE: 24-MAY-1995
CLASSITCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/036,210
FILING DATE: 23-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.3%; Score 14; DB 2;
100.0%; Pred. No. 1.5e-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: MISTOCK, S. Leellie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-025
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ. ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    357 VHCSAGVGRIGVFI 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 VHCSAGVGRIGVFI 314
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amino acid
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Patent No. 5952212
GENERAL INFORMATION
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COPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE: 23-MAR-1993
CLASSIFICATION UNMERS: US/08/036,210
FILING DATE: 23-MAR-1993
CLASSIFICATION: 435
ATTOREY/AGATT INFORMATION:
REPERRENCE/DOCKET NUMBER: 18,872
REPERRENCE/DOCKET NUMBER: 18,872
FELEPHONE: 212-790-9090
TELEFAN: 212-809-9190
TELEFAN: 212-909-9190
TELEFAN: 314: PENNIE
INPORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 898 amino acids
TTRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-036-210-22
Query Match
Best Local Similarity 100.0%; Pred. No. 3.2è-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 357 VHCSAGVGRTGVFI 370
Db 797 VHCSAGVGRTGVFI 810
Db 797 VHCSAGVGRTGVFI 810
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Sequence 1, Appli
Sequence 3, Appli
Sequence 8, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 22, Appli
Sequence 23, Appli
Sequence 24, Appli
Sequence 25, Appli
Sequence 5, Appli
Sequence 5, Appli
                                                                                                      June 16, 2004, 13:33:02; Search time 48 Seconds (without alignments) 2500.319 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1
Sequence 1
Sequence 5
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1 MSSPRKVRGKTGRDNDEEEG.....QVQFCYEIVLEVLQNLLALY
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1. (cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

1. (cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

1. (cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

1. (cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

1. (cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

1. (cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

1. (cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

1. (cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-095-478-2
US-09-095-478-2
US-09-095-478-6
US-09-095-478-4
US-09-095-478-4
US-09-095-478-22
US-09-095-478-22
US-09-095-478-24
US-09-095-478-24
US-09-095-478-24
US-10-117-1082
US-10-117-1082
US-10-314-191
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                                                                        - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Match Length
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146088844999
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No.
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ALIGNMENTS

Sequence 47, Appl	Sequence 27, Appl	e 11,	19	e 15,	950,	e 72	22,	12	54,	e 44	•	55,	o)	•	_	••	٠.	٠.	, ,	• •	•	Sequence 4, Appli	• • •	,	H	Sequence 6, Appli	9)	Sequence 47, Appl	• •	
US-10-314-232-47	US-09-788-626-27	US-10-31	US-10-40B	US-10-314-232-15	9-925-	. US-10-291-265-722	US-10-314-232-22	-10-258-666-1	US-09-808-602-54	US-09-800-198-4	US-10-29	US-09-808-602-55	₽	ns-:	US-1	ns-(US-10-673-8	US-1	US-10-087-	US-10	US-09-822-	US-10-673-	US-10-087	ر	3-788	US-09-788-626-6		US-10-3	US-10-408-765A-2747	
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289	294	322	344	401	442	647	888	1495	1502	1502	1907	1948	1948	2281	2281	2291	2291	2299	2300	2300	2301	2301	2302	2302	313	319	1216	1238	1329	
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14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	12	12	12	12	12	
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

RESULT 1

US-095-478-1

US-095-478-1

US-095-478-1

SEQUENCE 1, Application US/09095478

Publication No. US2003009597041

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
WUMBER TO SEQUENCES:
CORRESPONDENCE ADDRESS:
NUMBER TO SEQUENCES:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STREET: Suite 4700
CITY: Los Angeles
STREET: Suite 4700
CITY: Los Angeles
STREET: Suite STREET
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: Strange COMPUTER: Estabable FORM:
MEDIUM TYPE: Strange COMPUTER: Estabable FORM:
MEDIUM TYPE: Strange COMPUTER: Estabable FORM:
MEDIUM TYPE: Strange COMPUTER: READABLE FORM:
MEDIUM TYPE: Strange COMPUTER: NEADABLE FORM:
MEDIUM TYPE: Strange COMPUTER: NEADABLE FORM:
MEDIUM TYPE: Strange COMPUTER:
ME

OPERATING SYSTEM: IBM P.C. DOS SOFTWARE: FASESEG for Windows CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/095, FILING DATE: CLASSIFICATION: PRIOR APPLICATION NUMBER: FILING DATE: ATTORNEY/AGENT INFORMATION: NAME: Warburg, Richard J.

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFRENCE/DOCKET NUMBER: 224/115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600

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61 SFSDKYELVYPEPLESDIDEIVWDVSDRSLRANRWNSKDSETAGPSKTVSPVLSGSSRLSK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SFSDKYELVYPEPLESDIDETVWDVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 DIETSVSEKELTQLAQIRPLIFNSSARSAARDCLNTLQKKEELDIIREFLELEQMTLPDD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTVRVPQIVXXSTGKSQCVKHLQFTVWPDHGTPASADPPIXYVRYVRKSHITGPLLVHCS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FINSGNTI QNRDKORRYRDILDPYDSTRVPLGKNKDYINASYIRIVNHEEEFFYIAT QCPLPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 TIEDPWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLBPEHFSVPLETFHVTQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSSPRKVRGKTGRDNDEBEGNSGMLNLRNSLPSSSQKMTPTKPIFGNKMNSENVKPSHHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DTETSVSEKELTQLAQIRPLIFNSSARSAMRDCLNTLQKKEELDIIREFLELEQMTLPDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 AGVGRIGVPICVDVVPSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 405
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WENTION: NOVEL PROTEIN TYROSINE
VENTION: PHOSPHATASE SUPTPOS AND
VENTION: RELATED PRODUCTS AND
VENTION: METHODS
          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09095478
| Publication No. US20030095970A1
| GENERAL INFORMATION:
| TITLE OF INVENTION: PHOSPHATAND:
| TITLE OF INVENTION: PHOSPHATAND RITLE OF INVENTION: PHOSPHATAND RITLE OF INVENTION: METHODS
| VORRESPONDENCE ADDRESS:
| STREET: STREET: STREET: STREET: STREET: STREET:
| STREET: STREET: STATE 4700
| CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                   TELECOMOUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPRAX: (213) 955-0440
TELERAX: (213) 955-0440
TELEX: (67-3510
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
TYPE: amino acids
STREET: ACID NO: 3:
CHARACTERISTICS:
CHAR
                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: WARDING, RICHARD J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 22,
                                                                    APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 TIEDEWQMVLENNCHVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQY 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SFSDKYELVYPEPLESDTDETVWDVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIETSVSEKELTQLAQIRPLIFNSSARSAMRDCLMTLQKKEELDIIREFLELEQMTLPDD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIVRVPQIVKKSIGKSQCVKHLQPIKWPDHGIPASADFPIKYVRYVRKSHIIGPLLVHCS 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSSPRKVRGKTGRDNDEBEGGNSGNLNLRNSLPSSSGKMTPTKPIFGNKMNSENVKPSHHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SPSDKYELVYPEPLESDTDETVMDVSDRSLRNRMNSMDSETAGPSKTVSPVLSGSSRLSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 FTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRVVRKSHITGPLLVHCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSSPRKVRGKTGRDNDEEEGNSGNLNLRNSLPSSSQKWTPTKPIFGNKMNSENVKPSHHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 FNSGNTLQNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE SUPPROS AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
OCRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
CITY: LOS Angeles
STREET: Galifornia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          Cuery Match 100.0%; Score 426; I
Best Local Similarity 100.0%; Pred. No. 0;
Matches 426; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 51 Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09095478 Publication No. US20030095970Al GENERAL INFORMATION:
LENGTH: 426 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: Peptide
5-09-095-478-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||||||
||NLLALY 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLLALY 426
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3-09-095-478-3
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PHOSPHATASE SUPTPO5 AND
TITLE OF INVENTION: PHOSPHATASE SUPPROS
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORREST: 613 West Fifth Street
STREET: 613 West Fifth Street
STREET: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: Storage
COMPUTER: 
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APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WASTDUEG, RICHARD 32,327
REGISTRATION NUMBER: 32,327
REFERENCE/POCKET NUMBER: 224/
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDENESS: single
7 TOPOLOGY: linear
7 MOLECULE TYPE: Peptide
US-09-095-478-8
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 DIIREFLELEGMTLPDDFNSGNTLQNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIV 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 DIIREFLELEQMTLPDDFNSGNTLQNRDKNRYRDILPPYDSTRVPLGRANGYINASYIRIV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 NHEBRYFYIATQGPLPETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPL 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284 BPEHFSVFLETFHVTQYFTVRVFQIVKKSIGKSQCVKHLQFTKWPDHGTPASADFFIKYV 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321 EFEHFSVFLETFHVTQYFTVRVPQIVKKSTGKSQCVKHLQFTKMPDHGTPASADFFIKYV 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 RYVRKSHITGPLLVHCSAGVGRTGVFLCVDVVFSAIRKNYSFDIMNIVTQMRKQRCGMIQ 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 IFGNRANSENVKPSHHLSFSDKYELVYPEPLSSDTDETVWDVSDRSLRNRWNSMDSTAG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 PSKTVSPVLSGSSRLSKOTETSVSEKELFQLAQIRPLIFNSSARSAMRDCLNFLQKKEBL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Sequence 8, Application US/09095478
Sequence 8, Application US/09095478
Publication No. US20030095970A1
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
                                                                                                                                                                                                               CCMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Fast SEQ for Windows 2.0
CURRENT APPLICATION NUMBER: US/09/095,478
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PLING DATE:
                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/115
TELEPHONE: (213) 955-0440
TELEPHONE: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acids
STRANBENESS: single
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               California
                                                RY: U.S.A. 90071-2066
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285
                                                                                                 46 CHKWINSENVKPSHHLSFSDKYELVYPEPLESDTDETVWDVSDRSLRNRWNSMDSETAGPS 105
                                                                                                                                                                                             106 KTVSPVLSGSSRLSKDTETSVSEKELTQLAQIRPLIFNSSARSAMRDCLNTLQKKBELDI 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346 VRKSHITGPLLVHCSAGVGRIGVPICVDVVPSAIBKNYSFDIMNIVTQMRKQRCGMIQTK 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 EHPSVFLETFHUTQYPTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRY 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GNKGANSENVKPSHHLSFSDKYELVYPEPLESDTDETVWDVSDRSLRNRWNSMDSETAGPS
                                                                                                                                                                                                                                                                                                                                                                                       226 EEBYFYLATQGPLPETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEF
                                                                                                                                                                                                                                                                                                                                                                                                                   241 EHFSVPLETFHVTQYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRY
                                                                                                                                                                                                                         166 IREFLELEOMTLPDDFWSGWTLQNRDKWRYRDILPYDSTRVPLGKWKDYINASYIRIVNH
                                                     0; Gaps
Query Match 89.0%; Score 379; DB 10; Length 379; Best Local Similarity 100.0%; Pred. No. 0; Matches 379; Conservative 0; Mismatches 0; Indels
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241 KSTGKSQCVKHLQFTKWPDHGTPASADPFIKYVRYVRKSHITGPLLVHCSAGVGRTGVFI 300

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I: 122 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-095-478-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSTGKSQCVKHLQFTKWPDHGTPASADFF1KYVRYVRKSHITGPLLVHCSAGVGRTGVFI 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 LTQLAQIRPLIFNSSARSAMRDCLNTLQXXEELDIIREFLELEQMTLPDDFNSGNTLQNR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 DKARYRDILPYDSTRVPLGKAKDYINASYIRIVAHEERYFYIATOGPLPETIEDFWQMVL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 ENNCHVIAMITREIECGVIKCYSYWPISLKEPLBFEHFSVFLETFHVTQYFTVRVPQIVK 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
                                                                   Sequence 6, Application US/09095478
Publication No. US20030095970A1
GENERAL INFORMATION:
TITLE OF INVENTION: PHOSPHATASE SUPPOS AND
TITLE OF INVENTION: PROPERTY TYROSINE
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 83.1%; Score 354; DB Best Local Similarity 100.0%; Pred. No. 0; Matches 354; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.

ZIP: 90071-2066
COMPUTER READALEE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM D.C. DOS 5.0
SOFTWARE: FRASTEM: IBM P.C. DOS 5.0
SOFTWARE: PRASTEM: IBM P.C. DOS 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
FILING DATE:
CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 22/4/115
TELECOMMUNICATION:
NAME: WAIDLES, RICHARD J.
REGISTRATION NUMBER: 22/4/115
TELECOMMUNICATION INPORMATION:
TELEC
                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL PROTEIN
TITLE OF INVENTION: PHOSPHATASE STITLE OF INVENTION: RELATED PRODUCTIVE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: SLILE 4700
CITY: Los Angeles
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3-09-095-478-6
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6.1 RVFQIVKKSTGKSQCVKHLQFTKWPDHGTFASADFFIKYVRKYVRKSHIIGPLLVHCSAGV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 DFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DFWQMVLENNCNVIAMITREIBCGVIKCYSYWPISLKEPLEFEHFSVFLETFHVFQYFTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                    Sequence 4, Application US/0905478
Sequence 4, Application No. US20030095970A1
Sequence 10 No. US20030095970A1
GENERAL INFORMATION: PHOSEBATASE SUPTOS AND TITLE OF INVENTION: PHOSEBATASE SUPTOS AND TITLE OF INVENTION: PHOSEBATASE SUPTOS AND TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25
CORRESCONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 634 West Fifth Street
COMPUTER READABLE PORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: STORES
COMPUTER READABLE PORM:
MEDIUM TYPE: STORES
COMPUTER READABLE STORE
COMPUTER READABLE STORE
COMPUTER READABLE STORE
COMPUTER: IBM COMPATA:
MEDIUM TYPE: 3.5" DISKETTE, 1.44 Mb
MEDIUM TYPE: 3.40 Mb
MEDIUM TYPE: 3.40 Mb
MEDIUM TYPE: 3.40
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ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Comparible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Fastergr for Windows 2.0
SOFTWARENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: Peptide
                      California
U.S.A.
CITY: LOS
STATE: CI
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-095-478-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
        Sequence 22, Application US/09095478

Sequence 22, Application US/09095478

Publication No. US20030095970A1

GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: PHOSPHATASE SupPros.
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSES: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STREET: Suite 4700
CITY: Los Angeles
STREET: Galifornia
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5° Diskette, 1.44 MD
MEDIUM TYPE: 3.5° Diskette, 1.44 MD
MEDIUM TYPE: 3.5° Diskette, 1.44 MD
MEDIUM TYPE: SECORED
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-09-095-478-23
Sequence 23, Application US/09095478
Sublication No. US20030095970A1
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE SUPTPOS AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 TLPDDFNSGNTLQNRDKNRYRDILPYDSTR 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    : Lyon & Lyon
633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/ODCKET NUMBER: 224/
TELECOMMUNICATION INFORMATION:
TELEFACM (213) 489-1600
TELEFAC: (213) 955-0440
TELEFAC: (213) 955-0440
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: Peptide
-09-095-478-22
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Gaps
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Publication No. US20030095970A1

GENERAL INFORMATION:

APPLICANTON:

TITLE OF INVENTION:

METHODS

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSE:

ADDR
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5° Diskette, 1.44 Mb
MEDIUM TYPE: 5.5° DOS 5.0
SOFTWARE: FASTENG IBM P.C. DOS 5.0
SOFTWARE: FASTENG IBM P.C. DOS 5.0
SOFTWARE: FASTENG IBM P.C. DOS 5.0
SOFTWARE: FASTENG FOR WINGOWS 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
FILING DATE:
ATTONEY FASTENG ADDATE:
APPLICATION NUMBER: 32,327
REFERENCE/DOCKET NUMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSSPRKVRGKTGRDNDEEEGNSGNLNLRN 29
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5.4%; Score 23; DB 10; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.3e-14;
Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                     Length 29;
                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-09-095-478-5
Sequence 5, Application US/09095478
Publication No. US20030095970A1
GENERAL INPORMATION:
Publication No. US20030095970A1
GENERAL INPORMATION:
TITLE OF INVENTION:
PHOSPHATASE SUPPOS AND
TITLE OF INVENTION:
METHODS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEB: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: 613 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
COMPUTER: Suite 4700
CITY: Los Angeles
STATE: California
COUNTER: Suite 4700
CITY: Los Angeles
COMPUTER: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSM: IBM P.C. DOS 5.0
SOFTWARE: PASTSEM: IBM P.C. DOS 5.0
SOFTWARE: READABLE FORM:
MEDIUM TYPE: 31.5 "Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATION TYPE: 32.4718
FILING DATE:

                                                                                                                                             Query Match 6.8%; Score 29; DB 10; I
Best Local Similarity 100.0%; Pred. No. 6.9e-21;
Matches 29; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                   83 WDVSDRSLRNRWNSMDSETAGPSKTVSPV 111
                                                                                                                                                                                                                                                                                                                                                    1 WDVSDRSLRNRWNSMDSETAGPSKTVSPV 29
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear;
MOLECULE TYPE: Peptide
US-09-095-478-5
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-09-095-478-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
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US-10-311-764-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGULT 10
SGULT 10
SGULT 10
SGUGGE 25, Application US/09095478
Sequence 25, Application US/09095478
Publication No. US20030095970A1
GENERAL INFORMATION:
APPLICANT: PLOWER, GEOGRY
TITLE OF INVENTION: PHOSPHATASE SUPIPOS AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: ABTHOUS
NUMBER OF SEQUENCES: 25
CORRESSORS: Lyon & Lyon
STREET: Gailfornia
CONTRET: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER: IBM COMPATIBLE COMPATIBLE STATES: STA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 SPVLSGSSRLSKDTETSVSEKELTQLAQI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SPVISGSSRISKDTETSVSEKELTQLAQI 29
    FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGAT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 224/:
REFERENCE/DOCKET NUMBER: 224/:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEGUING TELECOMMUNICATION OF SEGUING TELECOMMUNICATION:
TELECOMMUNICATION OF SEGUING TELECOMMUNICATION OF SEGUING TELECOMMUNICATION OF SEGUING SEGUING ACIDS
TYPE: amilino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPDLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: Peptide 3-09-095-478-24
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// NAME/KEY: misc_feature
// LOCATION: (1)...(1105)
// OTHER INPORMATION: Xaa = any amino acid or other as shown in Table 3
US-10-296-115-1082
                                                                                                                                                                                                                                                                                                                                                                                                      1015 PLLVHCSAGVGRTGV 1029
                                                                                                                                                                                                                                                                                                                                    354 PLLVHCSAGVGRTGV 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357 VHCSAGVGRTGVFI 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 VHCSAGVGRTGVFI 116
                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-314-232-9
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TITLE OF INVENTION: No. US20040053248Alel Nucleic Acids and Polypeptides
TITLE OF INVENTION: No. US20040053248Alel Nucleic Acids and Polypeptides
TITLE OF INVENTION: No. US200406,115
CURRENT APPLICATION NUMBER: US/10/296,115
CURRENT APPLICATION NUMBER: US09/488,725
PRIOR APPLICATION NUMBER: US09/488,725
PRIOR APPLICATION NUMBER: US09/552,317
PRIOR FILING DATE: 2000-04-25
SEQ ID NOS: 1478
SEQ ID NO 1082
LENGTH: 1105
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Sequence 4, Application US/10311764
Publication No. US2004002345A1
GENERAL INFORMATION:
APPLICANT: BAUGHN, Mariah R.; DING, Li
APPLICANT: BAUGHN, Mariah R.; DING, Li
APPLICANT: BAUGHN, Mariah R.; DING, Li
APPLICANT: BALIOTY, Vicki S.; GANDHI, Ameena R.
APPLICANT: BALIOTY, Vicki S.; GANDHI, Ameena R.
APPLICANT: KEARNEY, Liam; LEE, Ernestine A.
APPLICANT: KEARNEY, Liam; LEE, Ernestine A.
APPLICANT: ARVIZU, Chandra S.; RAMKUMAL, Madhusudan A.
APPLICANT: REDDY, ROOPA M.; SANJANWALA, Madhusudan A.
APPLICANT: TRORNTON, Michael B.; TRIBOULEY, Catherine M.
APPLICANT: THORNTON, Mainder K.; YANG, Junming APPLICANT: THORNTON, Michael B.; TRIBOULEY, Catherine M.
APPLICANT: CHAMMAL, Narinder K.; YANG, Junming APPLICANT: CHAMMAL, Narinder K.; YANG, Junming APPLICANT: CHAMMAL, Narinder K.; YANG, Junming CURRENT FILING DATE: 2000-12-16
PRIOR PELICATION NUMBER: US 60/212,447
PRIOR PELICATION NUMBER: US 60/212,447
PRIOR PELICATION NUMBER: US 60/212,20
PRIOR APPLICATION NUMBER: US 60/212,20
PRIOR PELICATION NUMBER: US 60/212,17
PRIOR APPLICATION NUMBER: US 60/212,17
PRIOR PELICATION NUMBER: US 60/212,17
PRIOR APPLICATION NUMBER: US 60/212,17
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4.5%; Score 19; DB 16; Length 420;
Best Local Similarity 100.0%; Pred. No. 6.4e-10;
Matches 19; Conservative 0; Mismatches 0; Indels
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OTHER INFORMATION: Incyte ID No. US20040023245A1 7476861CD1
5-10-311-764-4
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Publication No. US20040053248A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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OTHER INFORMATION: Description of Artificial Sequence: amino acid sequence
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Sequence 9, Application US/10314232
Fublication No. US20030138932A1
GENERAL INFORMATION:
APPLICANT: MOLLER, KARIN B.
APPLICANT: WILLER, KARIN B.
APPLICANT: ULLRICH, AARI
ITTLE OF INVENTION: PTP-531: A NOVEL PROTEIN TYROSINE PHOSPHATASE
FILE REFERENCE: 038602/0686
CURRENT APPLICATION UNMERR: US/10/314,232
CURRENT PILING DATE: 12092-012-09
PRIOR APPLICATION NUMBER: US/09/361,096
PRIOR APPLICATION NUMBER: US/09/361,096
PRIOR APPLICATION NUMBER: US/09/361,096
PRIOR APPLICATION NUMBER: US/09/361,096
PRIOR PILING DATE: 1995-05-24
PRIOR PILING DATE: 1995-03-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 9
LENGTH: 176
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
TITLE OF INVENTION: KINASS IDENTIFIED WITH THE METHOD
FILE REPERENCE: 038602/1543
CURRENT FILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: US/10/334,143
PRIOR PILING DATE: 2001-12-31
NUMBER OF SEQ ID NOS: 207
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 191
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Length 1105;
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                                                         Indels
   3.5%; Score 15; DB 12; L
100.0%; Pred. No. 1.4e-05;
tive 0; Mismatches 0;
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US-10-334-143-191
Sequence 191, Application US/10334143
Sequence 191, Application US/10334143
GENERAL INFORMATION:
APPLICANT: GRIGORIEV, IGORY VACHESLAVOVICH
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Query Match
3.3%; Score 14; DB 14; Length 176;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps
OTHER INFORMATION: encoded by PCR fragment S-10-314-232-9
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earch completed: June 16, 2004, 13:38:58 ob time : 49 secs

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rivat.lipolyOundin; pivotein-Vivosin-Pivospiacase nouvalogy riris.
F;1108/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1114/Binding site: substrate phosphate (Arg) #status predicted
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Best Local Similarity
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                                                       June 16, 2004, 13:29:21 ; Search time 20 Seconds (without alignments) 2048.880 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                       - protein search, using sw model
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hypothetical prote protein-tyrosine-p protein-tyrosine-p protein-tyrosine-p protein-tyrosine-p protein-tyrosine-p hypothetical prote protein-tyrosine-p	ALIGNMENTS homolog DKFZp566K0524.1 - human (fragment)	revision 11-Jun-1999 #text_change 13-Aug-1999 ewes, H.W.; Gassenhuber, J.; Wiemann, S. ence Database, May 1999 0040 kidney; clone DKFZp566K0524	Note: DKFZp566K0524.1 Note: DKFZp566K0524.1 Superfamily: protein-tyrosine-phosphatase homology 161-379/Domain: protein-tyrosine-phosphatase homology <ptp> Query Match 4.5%; Score 19; DB 2; Length 398; Best Local Similarity 100.0%; Pred. No. 3.6e-11; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</ptp>		protein-tyrosine-phosphatase (EC 3.1.3.48) - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 22-Jun-1999 C;Accession: 138140 R;Moller, N.P.; Moller, K.B.; Lammers, R.; Kharitonenkov, A.; Sures, I.; Ullrich, A. Broc. Natl. Accad. Sci. U.S.A. 91, 7477-7481, 1994 A;Title: Src kinase associates with a member of a distinct subfamily of protein-tyrosine A;Reference number: 138140; MUID:94329538; PMID:7519780 A;Accession: 138140 A;Accession: 138140 A;Residues: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-1114 < ARES. A;Cross.references: EMEL:X79510; NID:9532055; PIDN:CAA56042.1; PID:9532056 C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-b) C;Scywords phosphoprotein monoester hydrolase; tyrosine-specific phosphatase F;25-304/Domain: protein 4.1 membrane-binding domain homology < AB41> F;25-304/Domain: protein-tyrosine-phosphatase homology < PTP2>
727722 7440169 7440169 156540 1156540 1125992 868250 868250 8742671 744267 744267 744267 744267 744267 744267 744267 744267	ALIGN	isio H. Dat	shosphatase ne-phosphats Score 19; Pred. No. 0; Mismatc	C 210	revision 31- revision 31- revision 31- Lammers, R.; 9 With a memb UID:94329538; ated from GB/ ated from GB/ ane-phosphatas hosphoric mon membrane-bind rosine-phosph
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=======================================	ryrosine	S: Homo 11-Jun- 10 - TO 1 - TO 10 - TO	DYZPSS66K0524.1 family: protein- 79/Domain: prote Match Local Similarity	192 K	tyrosine-phosphatase ss: Homo sapiens (man) 31-May-1996 #sequence, ion: I38140 it. N.P.; Moller, K.B.; itl. Acad. SSI. U.S.A. Src kinase associates nice number: I38140; M inn: I38140 inn: I38140 inn: I38140 inn: I38140; M inn: Inn: Inn: Inn: Inn: Inn: Inn: Inn:
0 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	RESULT 1 108716 Protein-tyrosine-phosphatase C.Shecies: Homo saniens (man)	C.jageacuses Homo saplems (man) C.jageacuses Homo saplems (man) C.jaccession: T08716 R.Amsorge, W.; Wirkner, U.; Mewes, submitted to the Protein Sequence A.jaccession: T08716 A.jaccession: T08716 A.jaccession: T08716 A.jaccession: T08716 A.jaccession: T08716 A.jaccession: T08716 A.jaccession: Man	A'Note: DKP2p566K0524 C'Superfamily: protein P;161-379/Domain: prot Query Match Best Local Similarii Matches 19; Cons	Oy Db RESULT 2	protein-tyrosine-phosphatase C.Species: Homo sapiens (man C.Species: Homo sapiens (man C.Species: Homo sapiens (man C.Species: Homo sapiens (may 1996 #sequenc. C.Accession: I38140 R.Moller, N.P.; Moller, K.B. Artle: Src Kinase associating Artle: Src Kinase associating Artle: Src Kinase associating Artle: Src Kinase associating Arcession: I38140 A.Scession: I38140 A.Status: preliminary; trans: A.Molecule type: mRNA A.Status: Preliminary; trans: A.Molecule type: mRNA A.Status: I-1174 «RES. C.Superfamily: protein-tyros: C.Superfamily: protein-tyros: C.Superfamily: protein-tyros: C.Stayords: phosphoprotean; P.55-304/Domain: protein-ty

3.5%; Score 15; DB 2; Length 1174; 100.0%; Pred. No. 1.4e-06;

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C;Keywords: glycoprotein; phosphorotein; phosphoric monoester hydrolase; transmembrane [F:1-582/Domain: leukocyte common antigen cytosolic domain homology (fragment) <LAC> F;50-27/Domain: protein-tyrosine-phosphatase homology <FPP1> F;50-27/Domain: protein-tyrosine-phosphatase homology <FPP1> F;233/Active site: Cys (phosphocysteine intermediate) #status predicted F;229/Anding site: substrate phosphate (Arg) #status predicted F;514/Active site: Cys (phosphocysteine intermediate) #status predicted F;514/Active site: cys (phosphocysteine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                     protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type f - mouse (fragment)
N.Alternate names: leukcoyte antigen-related protein LAR
().Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Accession: A57068; 540280
C.Accession: A57068; 540280
R.Schaapveld, R.O.J.; van den Maagdenberg, A.M.J.M.; Schepens, J.T.G.; Olde Weghuis, D.; Genomics 27, 124-130, 1995
R.A.Tile: The mouse gene Ptprf encoding the leukocyte common antigen-related molecule LAR
A.Tile: The mouse spene Ptprf encoding the leukocyte common antigen-related molecule LAR
A.A.Tile: The compared with conceptual translation
A.Solecule type: mRNA
A.Setatus: not compared with conceptual translation
A.Golecule type: mRNA
A.Golecule type
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C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; i
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submitted to the EMBL Data Library, March 1995
A;Description: Anlar-a transmembrane, receptor-like protein tyrosine phosphatase from the
A;Reference number: SS3089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: Ptprf
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: S40280
A;Accession: S40280
A;Molecule type: mRNA
A;Residues: 116-221 <HEN>
A;Cross-references: EMBL:Z23049; NID:g438135; PIDN:CAA80584.1; PID:g438136
C;Genetics:
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A;Residues: 1-1231 <SPI>
A;Cross-references: EMBL:X85217; NID:g732549; PIDN:CAA59483.1; PID:g732550
C;Genetics:
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100.0%; Pred. No. 7.6e-06;
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                                                                    Indels
                         Pred. No. 1.4e-06;
Mismatches 0;
100.08; PI
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                                                                    15; Conservative
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hes 14, Conservative
                         Best Local Similarity
Matches 15, Conserv
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ncogene 10, 407-414, 1995
;Title: Enhanced expression of multiple protein tyrosine phosphatases in the regenerati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-b
Keywords: phosphoprotein
25-304/Domain: protein 4.1 membrane-binding domain homology <B41>
                                                                                                                                                                                                                                                                                                                                                    Species: Rattus norvegicus (Norway rat); Pates 10-Apr-1996 #text_change 22-Jun-1999; Pacession: S51005; S5161 #text_change 22-Jun-1999; Pacession: S51005; S5161 #text_change 22-Jun-1999; Pacession: S51005; S5161 #text_change 22-Jun-1999; Pacession: S5105; S5161 #text_change 22-Jun-1999; Pacession: S5105; Banville, D.; Tong, Y.; Stocco, R.; Masson, S.; Ma, S.; Fantus, G.; Shen, Fatt. 356, 351-356, 1994; Pacesine phosphatase with sequence homology; Reference number: S51005; MUD:95104449; PMID:7805871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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Species: Mus musculus (house mouse)
Bate: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: S51161
Molecule type: mRNA
Residues: 840-1175 <LAB>
Cross-references: EMBL:U18293; NID:g603228; PIDN:AAA62154.1; PID:g603229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: mRNA
Residues: 1-1175 <LAA>
Cross-references: EMBL:U17971; NID:g662113; PIDN:AAA62153.1; PID:g602255
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1110/Active site: Cys (phosphocysteine intermediate) #status predicted
1116/Binding site: substrate phosphate (Arg) #status predicted
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Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: mRNA
Residues: 1-1176 <RES>
(Cross-references: GB:D37801; NID:g604885; PIDN:BAA07053.1; PID:g604886
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Pred. No. 1.4e-06;
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Reference number: 158345; MUID:95140431; PMID:7838537
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3.5%; Scc
Best Local Similarity 100.0%; Pi
Matches 15; Conservative 0;
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                                                                                                                                                                                1103 PLLVHCSAGVGRTGV 1117
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                                                                                                           354 PLLVHCSAGVGRTGV 368
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Genetics: <PTP2E1>
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Genetics: <PTP2E>
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667-1230/Domain: leukocyte common antigen cytosolic domain homology <LAC>
1047-1270/Domain: protein-tyrosine-phosphatase homology <PTP2>
931/Active site: Cys (phosphocysteine intermediate) #status predicted
1222/Active site: Cys (phosphocysteine intermediate) #status predicted
1222/Active site: Cys (phosphocysteine intermediate) #status predicted
1228/Binding site: substrate phosphate (Arg) #status predicted
Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase, transmembrane 208-293/Domain: fibronectin type III repeat homology <3FR> 619-1231/Domain: leukcyte common antigen cytosolic domain homology <LAC. 988-1211/Domain: protein-tyrosine-phosphatase homology <FFP> 872/Active site: Cys (phosphocysteine intermediate) #status predicted 1163/Active site: Cys (phosphocysteine intermediate) #status predicted 1169/Binding site: substrate phosphate (Arg) #status predicted
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Residues: 1-1290 <RES:
Cross-references: EMBL:X83505; NID:g732918; PIDN:CAA58495.1; PID:g732919
Longo, F.M.; Martignetti, J.A.; Le Beau, J.M.; Zhang, J.S.; Barnes, J.P.; Brosius, J.
Biol. Chem. 268, 26503-26511, 1993
Title: Leukocyte common antigen-related receptor-linked tyrosine phosphatase. Regulati
Reference number: 155393; MUID:94075340; PMID:8253779
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Residues: 831-1130 v RE2>
Cross-references: RMEL:100477; NID:g392565; PIDN:AAC04306.1; PID:g382566
Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ucocyte common antigen-related protein (LAR) - rat (fragment)
Alternate names: LAR receptor-linked tyrosine phosphatase
Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)
Species: Rattus norvegicus (Norway rat)
Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
Accession: A6493; 153393
Zhang, J.S.; Longo, F.M.
Cell Biol. 128, 415-431, 1995
Title: LAR tyrosine phosphatase receptor: alternative splicing is preferential theresesion: A56493; MUID:95146548; PMID:7844155
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100.0%; Pred. No. 1.6e-05;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                               Score 14; DB 2; Length ....
Pred. No. 1.5e-05;
0; Indels
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100.0%; Pred. No. ...
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Matches 14; Conservative
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Nes 14; Conservative
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procein-tyrosine-phosphatase (BC 3.1.3.48) - chicken cispecies allus (chicken) cispecies allus gallus (chicken) cispecies allus gallus (chicken) cibate: 13-Sep-1996 #text_change 21-Jan-2000 C.bate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000 C.scession: I50212 R.Scoker, A.W. M.W. Mech. Dev. 46, 201-217, 1994 A.Title: Isoforms of a novel cell adhesion molecule-like protein tyrosine phosphatase are A.Reference number: I50212 MJD:95001563; PMID:7918104 A.Accession: I50212 A.Scatus: preliminary; translated from GB/EMBL/DDBJ A.Molecule type: mRNA. A.Bolecule type: mRNA. A.Bolecule type: mRNA.
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F;245-299/Domain: immunoglobulin homology <IMM2>
F;245-299/Domain: immunoglobulin homology <IMM2>
F;217-399/Domain: immunoglobulin homology <IMM2>
F;217-399/Domain: fibronectin type III repeat homology <3FR>
F;114-1499/Domain: protein-tyrosine-phosphatase homology <FTP2>
F;1141/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1147/Binding site: substrate phosphate (Arg) #status predicted
F;1433/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1438/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                              C.Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; transme F;149-209/Domain: immunoglobulin homology <IMM1>
F;149-209/Domain: immunoglobulin homology <IMM2>
F;246-300/Domain: immunoglobulin homology <IMM2>
F;318-405/Domain: fibronectin type III repeat homology <FN3B>
F;411-504/Domain: fibronectin type III repeat homology <FN3B>
F;509-599/Domain: fibronectin type III repeat homology <FN3B>
F;600-684/Domain: fibronectin type III repeat homology <FN3B>
F;600-684/Domain: fibronectin type III repeat homology <FN3B>
F;800-1496/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1140/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1416/Finding site: substrate phosphate {Arg} #status predicted
F;1435/Finding site: substrate phosphate {Arg} #status predicted
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C,Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; 1
                                                                                                                                                                                                                                                                 C, Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
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A;Note: authors translated the codon TGC for residue 27 as Gly, GAG for residue 79 as Glr
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100.0%; Pred. No. 1.8e-05;
:ive 0; Mismatches 0; Indels
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es 14; Conservative
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                                                                                                                      1-1496 <PAN>
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                                        A, Status: preliminary
A, Molecule type: mRNA
A; Accession: A48758
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A; Molecule type: mRNA
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149-209/Domain: immunoglobulin homology <IPM1>
149-209/Domain: immunoglobulin homology <IPM1>
413-506/Domain: immunoglobulin homology <IPM1>
413-506/Domain: immunoglobulin homology <IPM1>
413-506/Domain: immunoglobulin homology <IPM1>
413-506/Domain: protectin type III repeat homology <3FR>
82-11501/Domain: protectin type III repeat homology <IPPI>
128-1481/Domain: protein-tyrosine-phosphatase homology <PFP1>
1142/Active site: Cys (phosphocysteine intermediate) #link PTP1 #status predicted il148/Binding site: substrate phosphate (Arg) #link PTP1 #status predicted il33/Active site: Cys (phosphocysteine intermediate) #link PTP2 #status predicted il33/Active site: Cys (phosphocysteine intermediate) #link PTP2 #status predicted il33/Active site: Cys (phosphocysteine intermediate) #link PTP2 #status predicted il33/Active site: Cys (phosphocysteine intermediate) #link PTP2 #status predicted il33/Balinding site: substrate phosphate (Arg) #link PTP2 #status predicted
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Residues: 1-1501 «WAL)
Residues: 1-1501 «WAL)
Notes-references: GB:L19933; NID:g310242; PIDN:AAA42309.1; PID:g310243
Notes: in Genbank entry RATTYRPHOS, release 113.0, the source is designated as Rattus r
Shang, W.R.; Hashimoto, N.; Abmad, F.; Ding, W.; Goldstein, B.J. designated as Rattus r
Ichem, J. 302, 39-47, 1994
Inche: Molecular cloning and expression of a unique receptor-like protein-tyrosine-pho
Reference number: S46216; MUJD:94347119; PMID:8068021
cotein-tyrosine-phosphatase (EC 3.1.3.48) 2B, splice form LAR - rat
Alternate names: leukocyte common antigen-related phosphatase
ispecies: Rattus norvegicus (Norway at)
ibate: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Jun-2000
iAccession: ISB148; S46718
walton, K.M.; Martell, K.J.; Kwak, S.P.; Dixon, J.B.; Largent, B.L.
iwanton, K.M.; Martell, K.J.; Kwak, S.P.; Dixon, J.B.; Largent, B.L.
iwan 11, 387-400, 1993
iTitle: A novel receptor-type protein tyrosine phosphatase is expressed during neurogen
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;Residues: 1-1501 <2H2.
;Crss-references: EMBi.il2329; NID:g294573; PIDN:AAC37657.1; PID:g294574
;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
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Residues: 1-1691 <MIZ>
Experimental source: harin
Note: sequence inconsistent with nucleotide translation
Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBIP:136537)
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Pred. No. 1.8e-05;
0; Mismatches 0; Indels
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Molecule type: mRNA
Residues: 1-398,799-1691 <MI2>
Experimental source: brain
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Status: preliminary
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"Seywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hydrologic signal sequence #status predicted <SIG>
F;1-26/Domain: signal sequence #status predicted <SIG>
F;1-26/Domain: signal sequence #status predicted <NIG>
F;1-186.) Product: protein-tyrosine-phosphatase #status predicted <NAT>
F;149-209/Domain: immunoglobulin homology <IFMI2>
F;146-200/Domain: immunoglobulin homology <IFMI2>
F;146-180/Domain: fibronectin type III repeat homology <FNI3>
F;131-499/Domain: fibronectin type III repeat homology <FNI3>
F;11-592/Domain: elucorecte common antigen cytoolic domain homology <IAC>
F;144-1863/Domain: leucorecte common antigen cytoolic domain: protein-tyrosine-phosphates homology <FPI1>
F;150/Active site: Cys (phosphocysteine intermediate) #status predicted
F;150/Binding site: substrate phosphate (Arg) #status predicted
F;180/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                C.Xeywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hydi P;42-95/Domain: immunoglobulin homology <IMM3> P;142-95/Domain: immunoglobulin homology <IMM3> P;114-196/Domain: fibronectin type III repeat homology <PN3A> P;1075-1691/Domain: fibronectin type III repeat homology <PN3A> P;1075-1691/Domain: protein-tyrosine-phosphatase homology <PTP2> P;133/Active site: Cys (phosphocysteine intermediate) #status predicted P;1339/Binding site: substrate phosphate (Arg) #status predicted P;1623/Active site: Cys (phosphocysteine intermediate) #status predicted P;1629/Binding site: substrate phosphate (Arg) #status predicted
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N.Alternate names: leukocyte common antigen-related phosphatase
C;Species: Rattus norvegicus (Norway rat)
C;Species: Artus norvegicus (Norway rat)
C;Accession: S46217; S51174; A49104
R;Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
Biochem, J. 302, 39-47, 1994
A;Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phosphateserence number: S46216; MUID:94347119; PMID:8068021
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A; Residues: 1-1788, 'G',1790-1863 (GOL)
A; Residues: 1-1788, 'G',1790-1863 (GOL)
A; Cross-references: EMBL:111587; NID:9205134; PIDN:AAC37656.1; PID:9205135
B; Yan, B; Grossman, A.; Wang, H; D'Sustachio, P.; Mossie, K.; Musacchio, J.M.; Silvennc
J. Biol. Chem. 268, 24880-24886, 1993
A; Title: A novel receptor tyrosine phosphatase-sigma that is highly expressed in the nerv
A; Reference number: A49104; WUID:94043351; PMID:8227050
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C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; )
A;Note: sequence extracted from NCBI backbone (NCBIN:136522, NCBIP:136524)
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
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A;Residues: 1-1863 ZZHA>
A;Crosidues: EMBL:Lil1587
R;Goldstein, B.J
Bubmitted to the EMBL Data Library, February 1993
A;Reference number: S51174
A;Accession: S51174
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C.; Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane; p.1-16/Domain: signal sequence #status predicted <SIG>P.17-1897/Product: leukocyte antigen-related protein #status predicted <MAT>P:17-1250/Domain: extracellular #status predicted <EXT>P:17-1250/Domain: immunoglobulin homology <IMM1>P:37-99/Domain: immunoglobulin homology <IMM2>P:35-290/Domain: immunoglobulin homology <IMM2>P:36-290/Domain: fimunoglobulin homology <IMM3>P:36-290/Domain: fibronectin type III repeat homology <FN3B>P:36-365/Domain: fibronectin type III repeat homology <FN3D>P:56-685/Domain: fibronectin type III repeat homology *FN3D>P:56-685/Domain: fibronectin type III repeat homology <FN3F>P:36-883/Domain: fibronectin type III repeat homology <FN3F>P:36-383/Domain: fibro
                                       A,Gene: GDB:PTPRF; LAR
A,Cross-references: GDB:120138, OMIM:179590
A,Map position: 1p34-1p34
C,Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
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NiAlternate names: leukocyte common antigen homolog
NiContains: protein-tyrosine-phosphatase (BC 3.1.3.48)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 23-Jul-1999
CiAccession: S46216; S23252; Ā41032; A33154
Rizhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
Biochem. J. 302, 39-47, 1994
A;Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phos
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A;Cross-references: EMBL:L11586; NID:g205132; PIDN:AAC37655.1; PID:g205133
A;Cross-references: EMBL:L11586; NID:g205132; PIDN:AAC37655.1; PID:g205133
R;Hashimoto, N: Zhang, W.R.; Goldstein, B.J.
B;Hashimoto, N: Zhang, W.R.; Goldstein, B.J.
A;Hashimoto, N: Zhang, W.R.; Goldstein, B.J.
A;Hitle: Insulin receptor and epidermal growth factor receptor dephosphorylation by three A;Reference number: S23126; MUID:92287069; PMID:1599438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fil25-1897/Domain: intracellular #status predicted <INT>
Fil25-1897/Domain: intracellular #status predicted <INT>
Fil26-1886/Domain: protein-tyrosine-phosphatase homology <PTP1>
Fil36-1866/Domain: protein-tyrosine-phosphatase homology <PTP1>
Fil36-1877/Domain: protein-tyrosine-phosphatase homology <PTP2>
Fil4-97,146-197,243-288/Disulfide bonds: #status predicted Fil4-97,11,956/Binding site: carbohydrate (Asn) (covalent) #status predicted Fil538/Active site: Cys (phosphocysteine intermediate) #status predicted Fil544/Binding site: substrate phosphate (Arg) #status predicted Fil829/Active site: Cys (phosphocysteine intermediate) #status predicted Fil835/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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A;Status: nucleic acid sequence not shown
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A;Residues: 1-1898 <Z
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245-299/Domain: immunoglobulin homology <IPM1>
245-299/Domain: immunoglobulin homology <IPM1>
217-399/Domain: immunoglobulin homology <IPM1A>
217-399/Domain: dibronectin type III repeat homology <FN3A>
1278-1894/Domain: leukccyte common attigen cytosolic domain homology <IPC>
1536/Active site: Cys (phosphocyteine intermediate) #status predicted
1532/Binding site: cys (phosphocyteine intermediate) #status predicted
1826/Active site: Cys (phosphocyteine intermediate) #status predicted
1832/Binding site: substrate phosphate (Arg) #status predicted
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Jake: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 22-Jun-1999
Accession: 503841; Jul0651
Streuli, M.; Krueger, N.X.; Hall, L.R.; Schlossman, S.F.; Saito, H.
Exp. Med. 168, 1523-1530, 1988
Title: A new member of the immunoglobulin superfamily that has a cytoplasmic region horseference number: Jul0651; MUID:89035978; PMID:2972792
                                                                                                                                                                                                                                                                                                                                                                                                                                             otein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form B precursor Alternate names: MPTP delta type B/C
Contains: protein tyrosine phosphatase, receptor type delta, splice form C
Species: Was musculus (house mouse)
Baceise: Apr-1995 #sequence_revision 19-May-1995 #text_change 12-Peb-1999
Accession: C54689; B54689
Mizuno, K.; Rasequan, X.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.
Cell. Biol. 13, 5513-5523, 1993
Title: MPTP delta, a putative murine homolog of MPTP delta, is expressed in specialize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
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Note: sequence inconsistent with nucleotide translation
Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBID:137487)
Accession: B54689
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Residues: 1-352,'H',354-535,'S',537-601,1002-1894 <MI2>
Experimental Source: brain; splice form C
Note: sequence inconsistent with nucleotide translation
Note: sequence extracted from NCBI backbone (NCBIN:136527, NCBIP:136530)
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Residues: 1-1897 <STR>
Cross-references: EMBL:Y00815; NID:g34266; PIDN:CAA68754.1; PID:g34267
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                                                     Indels
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    Pred. No. 2.3e-05; 
; Mismatches 0;
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100.08;
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Molecule type: mRNA
Residues: 1-1894 <MIZ>
    Best Local Similarity
Matches 14, Conserv
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Gaps

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Cross-references: GB:M60103, NID:g205130; PIDN:AAA41510.1; PID:g205131

**Pot. D.A.; Moodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.B.

thmitted to the Protein Sequence Database, December 1990

**Reference number: A33154

**Accession: A33154

**Molecule types mRNA

**Residues: 1035-1072,'8', 1074-1433,'T', 1435-1638,'N', 1640-1642,'HT', 1645-1898 <PO2>

**Comment: Only the first of the two domains homologous with protein-tyrosine-phosphatas
Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
3.3%; Score 14; DB 2; Length 1898;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels
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earch completed: June 16, 2004, 13:33:31 ob time : 21 secs

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InterPro; IPR000387; TYR phosphata InterPro; IPR000247; TYR PP. Pfam; PP001021 Y phosphatase; 1. Pfam; PP00102; Y phosphatase; 1. Pfam; PR00102; Y phosphatase; 1. PRINTS; PR00700; PRTYPHPHTASE. SWART; SW00295; B41; 1. SWART; SW00194; PTPc; 1. PROSITE; PS00660; FERM 1; 1. PROSITE; PS00661; FERM 2; 1.
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062728 rattus norv
062136 muse musculu
910586 homo sapien
013132 homo sapien
015678 homo sapien
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062130 mus musculu
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064455 mus musculu
064612 rattus norv
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064612 rattus norv
024456 homo sapien
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caenorhabdi
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1 MSSPRKVRGKTGRDNDEEDG.......QYQFCYBIVLBVLQNLLALY 426
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Copyright (c) 1993 - 2004 Compugen Ltd.
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PTNS_HUMAN
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CD45_MOUSE
PTPO_HUMAN
CD45_RAT
PTP9_DROME
CD45_RAT
PTPB_HUMAN
PTPG_CHICK
PTPB_CHICK
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Gapop 60.0 , Gapext 60.0
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Match Length DB
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P23471 Q62656 Q99952	P29461 sacchar P26045 homo se P80560 mus mus	002695	P35992	P725_STYPL P28217 styela plic	ALIGNMENTS		PRT; 1174 AA.	(ا	<pre>sequence update) annotation update)</pre>	Protein tyrosine phosphatase, non-receptor type 21 (EC 3.1.3.48)	e D1).		. Craniata, Vertebrata, Euteleostomi,	י כפרמודיודון יוסשדייינפטן ייסייי			MEDLINE=94329534; FUDMed=7519740; Moeller N.P.H., Moeller K.B., Lammers R., Kharitonenkov A., Sures I.,		with a member of a distinct sublamily of latases containing an ezrin-like domain.";	$91:7477-7481(1994)$.		Contains 1 FERM domain. Delongs to the protein-twrosine phosphatase family.	mc process cyrocastic processions and ly.	This SWISS-PROT entry is copyright. It is produced through a collaboration	of Bioinformatics and the EMBL outstatio	tions as long as its content is in no	and this statement is not removed. Usage by and for commercial	agreement (see nttp://www.lBb-sib.cm/ammom lsb-sib.ch)					GO:0004725; F:protein tyrosine phosphatase activity; TAS.	y rac ron;
	750 1 913 1 1001 1						STANDARD;	Creat	35, Last	hosphatas	phosphatase	п).	Chordata; Chimates;	i ritimore		scle;	Fubmed=/5.		ates with hosphatas	Proc. Natl. Acad. Sci. U.S.A. 91	+ phosphate.	ntains 1	Non-receptor class subfamily	try is col	Institut	t institu	statement	a license o license	EMBL, X79510; CAA56042.1; DID: 138140: 138140	; .	PTPN21.	cytoskele	protein t	procein a
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein tyrosine phosphatase, non-receptor type 21 (EC 3.1.3.48)
Protein-tyrosine phosphatase 2B).
Protein-tyrosine phosphatase 2B).
Protein-tyrosine phosphatase Rel. (EC 3.1.3.48)
Previous norregicus (Rat).
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PHOSPHOCYSTEINE INTERMEDIATE
(BY SIMILARITY).
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                               340 343 POLY-PRO.
565 574 POLY-RO.
1174 AA; 133287 MW; 5772D9B1A99B3FDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                      Score 15; DB 1; Le
Pred. No. 3.5e-07;
PROSITE; PSS0057; FERM 3; 1.
PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
PROSITE; PS50055; TYR_PHOSPHATASE 2; 1.
STRUCTURAL PICOCEALI, CYLORKELECOR; Hydrolase.
DOMAIN 23 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1175 AA.
                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q62728-2; Sequence=VSP_000498,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q62728-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 1 AND 2B).
                                                                                                                                                                                                                                                                                          3.5%; Scc...
100.0%; Pred
0; N
                                                                                                                                                                                                                                                                                                                                                                                                                                     1103 PLLVHCSAGVGRTGV 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U17971; AAA62153.1; -.
EMBL; U18293; AAA62154.1; -.
                                                                                                                                                                                                                                                                                                                                                                                            354 PLLVHCSAGVGRTGV 368
                                                                                                                                                                                                                                                                                   Query Match
Beet Local Similarity 100...
Thes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tyrosine + phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE PRODUCTS
                                                                                                                                      1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U18293; AAA621
PIR; S51005; S51005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                      921
1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=1;
                                                                                                                                                                                                                                             DOMAIN
SEQUENCE
                                                                                                                                                      ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PINL RAT
                                                                                                             DOMAIN
                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESULT 2
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HSSP; Q06124; 2SHP. InterPro; IPR000299; Band_4.1. InterPro; IPR000387; TYR_phosphatase.

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0
                           Ream, PP00102; Y Ducor-
R PEAM; PR00102; Y Ducor-
R PRINTS; PR00035; BAND41.
R PRINTS; PR00035; BAND41.
DR PROSTITS; S000660; PREM 1; 1.
DR PROSTITS; PS00661; FERM 2; 1.
DR PROSTITS; PS00657; FERM 3; 1.
DR PROSTITS; PS00657; FERM 3; 1.
DR PROSTITS; PS00655; TYR PHOSPHATASE 1; 1.
DR PROSTITS; PS00655; TYR PHOSPHATASE 2; 1.
DR PROSTITS; PS00656; TYR PHOSPHATASE 2; 1.
DR PROSTITS; PS00665; TYR PHOSPHATASE 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=CSTBL/6; TISSUE=Liver;
MEDLINE=95140431; PubMed=7838537;
Higashitsuil H., Arri S., Furutani M., Imamura M., Kaneko Y.,
Higashitsuil H., Arri S., Furutani M., Imamura M., Kaneko Y.,
Takenawa J., Nakayama H., Fujita J.;
"Enhanced expression of multiple protein tyrosine phosphatases in the regenerating mouse liver: isolation of PTP-RL10, a novel cytoplasmic-type phosphatase with sequence homology to cytoskeletal protein 4.1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- FUNCTION: May be involved in the regulation of growth and differentiation of liver cells.
--- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tyrosine + phosphate.
--- Tiscule Specificity: Liver.
--- SIMILARITY: Contains 1 PERM domain.
--- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein tyrosine phosphatase, non-receptor type 21 (BC 3.1.3.48)
(Protein-tyrosine phosphatase PTP-RL10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           % Match 3.5%; Score 15; DB 1; Length 1175; Local Similarity 100.0%; Pred. No. 3.5e-07; nes 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN-TYROSINE PHOSPHATASE.
PHOSPHOCYSTEINE INTERMEDIATE
{BY SIMILARITY}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1175 AA; 133411 MW; 82A684FIC0F5ECF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Missing (in isoform 2E). /FTId=VSP 000498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1176 AA
                        Pfam; PF00373; Band 41; 1.
Pfam; PF00102; Y phosphatase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1104 PLLVHCSAGVGRTGV 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 PLLVHCSAGVGRTGV 368
InterPro; IPR000242; Tyr_PP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oncogene 10:407-414 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              839
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Q62136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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us-09-095-478a-5.0li.rsp

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MEDLINE=90046860; PubMed=2554325;
Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;
A family of receptor-linked protein tyrosine phosphatases in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90316093; PubMed=1695146; Strenli M., Krueger N.X., Thai T., Tang M., Saito H.; Krueger N.X., Thai T., Tang M., Saito H.; Publinct functional Rose of the two intracellular phosphatase like domains of the receptor-linked protein tyrosine phosphatases LCA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=899335978; PubMed=2972792; Streuli M., Krueger N.X., Hall L.R., Schlossman S.F., Saito H.; Anew member of the immunoglobulin superfamily that has a cytoplasmic region homologous to the leukocyte common antigen."; Exp. Med. 168:1523-1530(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
LAR protein precursor (Leukocyte antigen related) (EC 3.1.3.48).
PTPRF OR LAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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; Pred. No. 3.5e-07;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN-TYROSINE PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1176 AA; 133490 MW; 529FBE22F1335B75 CRC64;
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                                                                                                                                                                                                          Pfam; PF00173; LROUGL41; IT. F.
Pfam; PF00173; Band 41; I.
Pfam; PF00102; Y_phosphatase; I.
PRINTS; PR00700; PRTYPHPHTASE.
SMART; SM00295; BAND41.
SMART; SM00194; PTPC; I.
PROSITE; PS00660; FERM 1; I.
PROSITE; PS00661; PERM 2; I.
PROSITE; PS00661; PERM 2; I.
PROSITE; PS00061; PERM 2; I.
PROSITE; PS00065; TYR PHOSPHATASE I; I.
PROSITE; PS00056; TYR PHOSPHATASE 2; I.
SKINGLURAL PS00056; TYR PHOSPHATASE 2; I.
SKINGLURAL PS00066; TYR PHOSPHATASE 2; I.
PROSITE; PS00066; TYR PHOSPHATASE 2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1897 AA.
EMBL, D37801, BAA07053.1; -.
PIR, 15844; 158345.
HKSP, P29350, 1GWZ.
MGD, MGI:1344466, Ptpn21.
InterPro; IPR000299, Band 4.1.
InterPro; IPR000397; TXR_phosphatase.
InterPro; IPR000242; TYR_PP0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY - PRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354 PLLVHCSAGVGRTGV 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBO J. 9:2399-2407(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
nes 15, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343
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MUTAGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                      MIN; 179590; ...

GO; GO:010058B7; C:integral to plasma membrane; TAS.

GO; GO:010058B7; C:integral to plasma membrane; TAS.

GO; GO:01005115; P:etalsmembrane receptor protein tyrosine pho. ..; TAS.

GO; GO:0107115; P:etalsmembrane receptor protein tyrosine pho. ..; TAS.

InterPro; IPR00395; FN III-like.

InterPro; IPR003962; FN III-like.

InterPro; IPR003191; IG-like.

InterPro; IPR003191; IG-like.

InterPro; IPR003191; IG-like.

InterPro; IPR003197; TYR_phosphatase.

InterPro; IPR003197; TYR_phosphatase.
                                                                             first one.
CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                       FUNCTION: The first PTPAse domain has enzymatic activity, while the second one seems to affect the substrate specificity of the
FUNCTION: It is possible that DLAR is a cell adhesion receptor. It possesses an intrinsic protein tyrosine phosphatase activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R InterPro; IPRU0021; fin3; 7.

R Pfam; PF00041; fin3; 7.

R Pfam; PF00041; fin3; 7.

R Pfam; PF00012; Yphosphatese; 2.

PRINTS; PR00700; FRTYPHPHTASE.

DR PRINTS; PR00700; PRTYPHPHTASE.

DR SWART; SW00194; PTPC; 3.

DR SWART; SW00194; PTPC; 3.

DR SWART; SW00194; PTPC; 3.

DR SWART; PR00194; PTPC; 3.

DR PROSITE; PS00383; TYR PHOSPHATASE 1; 2.

DR PROSITE; PS00383; TYR PHOSPHATASE 2; 2.

DR PROSITE; PS00055; TYR PHOSPHATASE 2; 2.

DR PROSITE; PS00055; TYR PHOSPHATASE PTP; 2.

PROSITE; PS00055; TYR PHOSPHATASE PTP; 2.

DR PROSITE; PS00055; TYR PHOSPHATASE PTP; 2.

""A*^nlase; Receptor; Glycoprotein; Signal; Transmembrane;
""A*nlase; Receptor; Glycoprotein; Signal; Repeat; 3D-structure.
                                                                                                        (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHOCYSTEINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
PROTEIN-TYROSINE PHOSPHATASE 1.
PROTEIN-TYROSINE PHOSPHATASE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C->S: LOSS OF ACTIVITY.
W: 439850F1D5C031FF CRC64;
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EXTRACELLULAR (POTENTIAL)
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N-LINKED (GLCNAC. . .)
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N-LINKED (GLCNAC. . .)
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                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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Σ
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285 28
711 71
956 99
11538 153
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CARBOHYD
MUTAGEN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
DOMAIN
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CARBOHYD
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1842 VHCSAGVGRTGVPI 1855
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENEMS outstation the European Bioinformatics Institute. There are extrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-1178.
MEDLINE-95204468; PubMed=7896816;
Pulido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M.;
Molecular characterization of the human transmembrane protein-
tyrosine phosphatase delta. Evidence for tissue-specific expression of alternative human transmembrane protein-tyrosine phosphatase delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Krueger N.X., Streuli M., Saito H.;
Krueger N.X., Streuli M., Saito H.;
"Structural diversity and evolution of human receptor-like protein
"Structural diversity and evolution of human receptor-like protein
tyrosine phosphates protein tyrosine phosphate + H(2)0 = protein
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISOIG==213e0-1,
Name=2; Synonyms=Ridney;
ISOIG==23466-2; Sequence=VSP_005147, VSP_005148, VSP_005149;
ISOIG=223466-2; Sequence=VSP_005150;
ISOIG=223468-3; Sequence=VSP_005169;
ISOIG=223468-3; Sequence=VSP_005169;
ISOIG=23468-3; Sequence=VS
                                                                                                                                                                                                                                                                  01-NOV-1991 (Rel. 20, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein-tyrosine phosphatase delta precursor (EC 3.1.3.48) (R-PTP-
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                              .
    3.3%; Score 14; DB 1; Length 1897; 100.0%; Pred. No. 6.4e-06; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 601598; -.
GO; GO:0005887; C:integral to plasma membrane; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine + phosphate.
--- SUBCELLULAR LOCATION: Type I membrane protein.
--- ALTERNATIVE PRODUCTS:
--- Event **Alternative splicing; Named isoforms**3;
Comment**Additional isoforms seem to exist;
                                                                                                                                                                                                                                 PRT; 1912 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 270:6722-6728(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91006018; PubMed=2170109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 390-1912 FROM N.A. TISSUE=Placenta;
                                                                                                                          1827 VHCSAGVGRTGVFI 1840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L38929; AAC41749.1; -. BEMBL; KS4131; CAA38068.1; -. PIR; A56178; A56178. HSSP; P18052; 1YFO.
                                                                                    357 VHCSAGVGRTGVFI 370
Query Match
Best Local Similarity 100.0
Matches 14; Conservative
                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:9668; PTPRD.
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . .; TAS. GO; GO:0005400; P:protein amino acid dephosphorylation; TAS. GO; GO:0006410; P:protein amino acid dephosphorylation; TAS. InterPro; CO:0007185; F:transmembrane receptor protein tyrosine pho. . .; TAS. InterPro; IPR008957; FN III-like.

InterPro; IPR0013961; FN III.

InterPro; IPR0013962; PnIII subd.

InterPro; IPR001398; Ig_c.

InterPro; IPR0013598; IfR_C.

InterPro; IPR0013598; IfYE_DP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 R AIRCETCU; INTOUCALE; ATLEET.

R AIRCETCU; INTOUCALE; ATLEET.

R PÉRM; PF00041; fül; 8.

R PÉRM; PF00047; igj 3.

R PÉRM; PF00014; FNIYPERII.

R RINTS; PR00014; FNIYPERII.

R SNART; SM00194; PTPC; 2.

SMART; SM00194; PTPC; 2.

SMART; SM00194; PTPC; 2.

R RART; SM00194; PTPC; 3.

R RART; SM0194; PTPC; TPPC; 
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Missing (in isoform 3).
Missing (in isoform 5).
R-sh: 2.5-POLD REDUCTION IN CLEAVAGE.
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N-LINKED (GLCNAC. .) (POTENTIAL),
N-LINKED (GLCNAC. .) (POTENTIAL),
N-LINKED (GLCNAC. .) (POTENTIAL),
M-LINKED (GLCNAC. .) (POTENTIAL),
Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN-TYROSINE PHOSPHATASE DELTA.
EXTRACELLULAR (POTENTIAL).
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PROTEIN-TYROSINE PHOSPHATASE 2.
PHOSPHOCYSTEINE INTERMEDIATE (BY
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100.0%; Pred. No. 6.Se-06;
tive 0; Mismatches 0; Indels
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FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 7.
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CYTOPLASMIC (POTENTIAL).
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IG-LIKE C2-TYPE 2.
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HGNC:9681; PTPRS.
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SEQUENCE OF 1-126 FROM N.A.
Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
Lamerdin J.E., McCready P.M., Dias J., Ramirez M., Stilwagen S.,
Phan H., Valasco N., Do L., Regala W., Terry A., Garnes J.,
Danganan L., Erler A., Christensen M., Georgescu A., Avila J.,
Lattix C., Andredise T., Trankheim M., Amico-Keller G., Coeffield J.,
Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
Arellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,
Olsen A.S., Carrano A.V.;
Sequence analysis of a 2.5 Mb region in 19913.3.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUB=Fetal brain;
MEDILNE=56120179; PubMed=6524829;
MEDILIAE=56120179; PubMed=6524829;
Pulido R., Serra-Bages C., Tang M., Streuli M.;
"The LAR/PTP delta/PTP signa subfamily of transmembrane protein-
tyrosine-phosphatases: multiple human LAR, PTP delta, and PTP signa
isoforms are expressed in a tissue-specific manner and associate with
the LAR-interacting protein LIP.1.",
Proc. Natl. Acad. Sci. U.S.A. 92:11686-11690(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISOId=013332-5; Sequence-VSP 050023, VSP 050025; TISSUE SPECIFICITY: DEtected in all tissues tested except for placente and liver.
SIMILARITY: BELONGS TO THE RECEPTOR CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE PAMILY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92119637; PubMed=1370651;
Adachi M., Sekiya M., Arimura Y., Takekawa M., Itoh F., Hinoda Y.,
Adachi M., Sekiya M., Arimura Y., Takekawa M., Itoh F., Hinoda Y.,
Imai K., Yachi A.,
"Protein-tyrosine phosphatase expression in pre-B cell NALM-6.";
Cancer Ree. S2:737-740(1992).
-:- FUNCTION: Interacts with LAR-interacting protein LIP.1.
-:- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=96255038; PubMed=8992885;
Endo N., Rutledge S.J., Opas E.E., Vogel R., Rodan G.A., Schmidt A.;
Human protein tyrosine phosphatase-sigma: alternative splicing and inhibition by bisphosphonates.
            01332; 015718; 016341;
10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Receptor-type protein-tyrosine phosphatase S precursor (EC 3.1.3.48)
(R-PTP-S) (Protein-tyrosine phosphatase sigma) (R-PTP-sigma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q13332-3; Seguence=VSP_050022, VSP_050026, VSP_050027;
                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Contains 3 immunoglobulin-like C2-type domain. SIMILARITY: Contains 8 fibronectin type III domains. SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tyrosine + phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
Brent-Alternative splicing; Named isoforms=5;
Comment=Additional isoforms seem to exist;
 PRT; 1948 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=PTPS-MEA;
IsoId=Q13332-2; Sequence=VSP_050021;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q13332-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bone Miner. Res. 11:535-543(1996).
   STANDARD;
                                                                                                                                sapiens (Human)
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   HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor protein tyrosine pho. . .; TAS.
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SMART; SM00194; PTPC; 2.
SMART; SM00194; PTPC; 2.
SMART; SM00194; PTPC; 2.
PROSITE; PS50085; ITR_PHOSPHATASE_1; 2.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
Cell adhesion; Immunoglobulin domain; Alternative splicing; Repeat.
SIGNAL 30 1948 RECEPTOR-TYPE PROTEIN-TYROSINE
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PIBRONECTIN TYPE-III 2.
PIBRONECTIN TYPE-III 3.
PIBRONECTIN TYPE-III 4.
PIBRONECTIN TYPE-III 4.
PIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 7.
PIBRONECTIN TYPE-III 7.
PIBRONECTIN TYPE-III 7.
PROPERIN-TYROSINE PHOSPHATASE 1.
PROTEIN-TYROSINE PHOSPHATASE 2.
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EXTRACELLULAR (POTENTIAL)
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
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GRIEW, FORNCISOLI, FIRES.

MIM, 601576, --
GO, GOUGOSGO, CINTERZAL TO plasma mer
GO, GO: 0005001; FIRENSEEMDRAIN ECCEPTO)
INCEPPO: IPRO08957; FN III-like.
INCEPPO: IPRO08957; FN III-like.
INCEPPO: IPRO0110; IG-like.
INCEPPO: IPRO0110; IG-like.
INCEPPO: IPRO0110; IG-like.
INCEPPO: IPRO0110; IG-like.
INCEPPO: IPRO01299; TYR_phosphatase.
INCEPPO: IPRO0242; TYR_PP.
INCEPPO: IPRO0242; TYR_PP.
INCEPPO: IPRO044; IG-like.
INCEPPO: IPRO044; IG-like.
INCEPPO: IRROPORTO, IRROPENTARE.
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EMBL; U40317; AAC50567.1; -.
EMBL; AC005790; AAC62832.1; -
EMBL; S708080; AAB21146.2; -.
HSSP; P18052; 1YFO.
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HSSP; P29350; 1GWZ.
Genew; HGNC:9647; PTPN14.
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ID PTNE MOUSE
AC Q62130;
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  OR REPORT OF THE PROPERTY OF T
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T -> HP (IN REF. 2).
SA -> RP (IN REF. 2).
GAEGRGPR -> RRARGERS (IN REF. 2).
GAEGRGPR -> RRARGERS (IN REF. 2).
R -> P (IN REP. 2).
R -> P (IN REP. 2).
TV -> SL (IN REF. 2).
F -> S (IN REF. 2).
F -> S (IN REF. 2).
V -> A (IN REF. 4).
V -> A (IN REF. 4).
V -> A (IN REF. 4).
N -> K (IN REF. 2).
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TISSUB=Breast carcinoma;
MEDLINE=95251727; PubMed=7733990;
Smith A.L., Mitchell P.J., Shipley J., Gusterson B.A., Rogers M.V.,
Crompton M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Pez: a novel human cDNA encoding protein tyrosine phosphatase- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)
(Protein-tyrosine phosphatase pez).
(Protein-tyrosine phosphatase pez).
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Missing (in isoform PTPS-F4-7), /PTId=VSP_050023.
                                                  dissing (in isoform PTPS-MEC).
/PTId=VSP 050024.
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Pred. No. 6.6e-06;
                                                                                                                                /FTId=VSP 05025.
Missing (In isoform PTPS-MEB).
/FTId=VSP 050026.
S -> G (In isoform PTPS-MEB).
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1948 AA; 217080 MW;
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Q15678;
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STRAIN=CB-17-SCID; TISSUE=Thywus;
MEDLINE=943.54645; PubMed=8074693;
MEDLINE=943.54645; PubMed=8074693;
"CDNA cloning of a novel protein tyrosine phosphatase with homology to cytoskeletal protein 4.1 and its expression in T-lineage cells.";
Biochem. Biophys. Res. Commun. 203:479-484(1994).
-i. FUNCTION: MAY BE INVOLVED IN THE REGULATION OF T CELL DEVELOPMENT.
-i. CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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-!- SIMILARITY: Contains 1 FERM domain.
-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)
Protein tyrosine phosphatase PTP36).
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100.0%; Pred. No. 0.00054;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                       PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).
POLY-PRO.
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Les 12; Conservative
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   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Protein-tyrosine phosphatase eta precursor (BC 3.1.3.48) (R-PTP-eta)

(HPTP beta-like tyrosine phosphatase) (Protein-tyrosine phosphatase receptor type J) (Susceptibility to colon cancer-1).

Mus musculus (Mouse).

Bukaryota; Metaron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamamoto T.,
"Molecular cloning and characterization of Byp, a murine
"Molecular cloning and characterization of Byp, a murine
receptor-type tyrosine phosphatase similar to human DEP-1.";
FEBS Lett. 378:7-14(1996)
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine + phosphate.
--- SUBCRILULAR LOCATION: Type I membrane protein.
--- TISSUB SPECIFICITY: Expressed in every tissue examined.
--- SIMILARITY: Contains I protein-tyrosine phosphatase domain.
--- SIMILARITY: Contains 6 fibronectin type III domains.
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                                                                                                                                                                                                                                                                                                                                                           PROTEIN-TYROSINE PHOSPHATASE.
PHOSPHOCYSTEINE INTERMEDIATE
(BY SIMILARITY).
POLY-PRO.
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 12; DB 1; Length 1189;
Pred. No. 0.00054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=MRT.-LIPR/LOS/UP.N.
MEDIINE=9614.069; PubMed=8549806;
Kuramochi S., Matsuda S., Matsuda Y., Saitoh T., Ohsugi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                566 573 POLITERO.
635 639 POLY-GLY.
712 718 POLY-GLU.
1189 AA; 135030 MW; 2B65B85F9C723303 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                    PISSP, J023551, 28HP.

MGD; MGI.102467, PEDDI4.

INTERFO; IPR0000299; Band 4.1.

INTERFO; IPR0000299; TYR_phosphatase.

InterPro; IPR000245; TYP_PP.

Pfam; PF00102; Y_phosphatase; 1.

Pfam; PF00102; Y_phosphatase; 1.

PRINTS; PR00935; BAND41.

PRINTS; PR00935; BAND41.

PRINTS; PR00035; PRINTPHPHTASB.

SMART; SM00194; PTPC; 1.

PROSITE; PS00660; PERM 1; 1.

PROSITE; PS00661; PERM 2; 1.

PROSITE; PS00389; TYR_PROSPHATASE 1; 1.

PROSITE; PS00389; TYR_PROSPHATASE 2; 1.

PROSITE; PS00389; TYR_PROSPHATASE 2; 1.

PROSITE; PS00389; TYR_PROSPHATASE 2; 1.

PROSITE; PS00565; TYR_PROSPHATASE 2; 1.
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                                                           EMBL; D31842; BAA06628.1; -
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| PTPJ_MOUSE
| Q64455;
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Matches
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FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 6.
                                                                                                                                                                                                                                             EMEL: D45212; BAA08146.1; ...

RESP: 18052; 1YPO.

RGD: G0:0001570; P:beart development; IMP.

R InterPro: IPR003957; PN III-like.

RICETPRO: IPR003987; TYR_Biosphatase.

InterPro: IPR00342; TYR_PP.

R FEan; PP00102; Y_Dhosphatase: 1.

R RINTS; PR00700; PR17PHPHTASE.

R PRNAT; SM00100; PN15.

R RNART; SM0194; PTPc: 1.

R RNOSITE; PS00056; TYR_HOSPHATASE 1; 1.

R RNOSITE; PS00056; TYR_HOSPHATASE 2; 1.

R RNOSITE; PS0056; TYR_HOSPHATASE 2; 1.

R RNOSITE; PS00056; TYR_HOSPHATASE 2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell growth.

CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.

Lyrosine + phosphate.

SUBCELLUAR LOCATION: Type I membrane protein.

PTM: N- and O-glycosylated.

DISEASE: Defects in PTPRJ are found in cancers of colon, lung, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22084388; PubMed=12089527;
Ruivenkamp C.A.L., van Wezel T., Zanon C., Stassen A.P.M., Vlcek C., Stivenkamp C.A.L., van Wezel T., Zanon C., Stassen A.P.M., Vlcek C., Scikos T., Klous A.M., Tripodis N., Perrakis A., Boerrigter L., Groot P.C., Lindeman J., Mooi W.J., Meijjer G.A., Scholten G., Dauwerse H., Paces V., van Zandwijk N., van Ommen G.J.B., Demant P., Ptprj is a candidate for the mouse colon-cancer susceptibility locus Scci and is frequently deleted in human cancers.";
Nat. Genet. 31:295-300 (2002).
--- FUNCTION: May contribute to the mechanism of contact inhibition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95086212; PubMed=7994032;
Honda H., Inazawa J., Nishida J., Yazaki Y., Hirai H.;
"Molecular cloning, characterization, and chromosomal localization of
a novel protein-tyrosine phosphatase, HPTP eta.";
Blood 84:4186-4194(1994).
                                                                                                                                                                                                                                                                                             012913; 015255; 08NHMZ; 08NHMZ; 015075...
01-NOV-1997 (Rel. 35, Created)
10-OCT-2003 (Rel. 42, Last agreence update)
Protein-tyrosine phosphatase eta precursor (EC 3.1.3.48) (R-PTP-eta)
(HPTP eta) (Protein-tyrosine phosphatase receptor type J) (Density PTPA, OR DEPL.) (CD148 antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=55024024; PubMed=7937872;
Oestman A., Yang Q., Tonks N.K.;
Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase,
is enhanced with increasing cell density.";
Proc. Natl. Acad. Sci. U.S.A. 91:9680-9684(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                               (POTENTIAL).
(POTENTIAL).
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                                                                                                       2.8%; Score 12; DB 1; Length 1238; 100.0%; Pred. No. 0.00056; Ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 33-1337 FROM N.A., AND VARIANTS COLON CANCER
                                                                              MW; 939479EDC8016835 CRC64;
                               (GLCNAC. . .)
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                                                                                                                                           12; Conservative
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1238 AA;
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                                                                                                                          Similarity
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RO; GO:0005001; F:transmembrane receptor protein tyrosine pho. .;

RO; GO:0005001; F:transmembrane receptor protein tyrosine pho. .;

RO; GO:0005767; P:call-cell signaling; TAS.

RO; GO:0007169; P:protein amino acid dephosphorylation; TAS.

RO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .;

RICEPTO; IPRO00367; FW_III-like.

RICEPTO; IPRO00367; FW_III-like.

RICEPTO; IPRO00367; TYR_phosphatase.

RICEPTO; IPRO00367; TYR_phosphatase.

REPTO; PRO00101; Yphosphatase.

REPTO; PRO00101; Yphosphatase.

REPTO; ROWOTO00; PRITYHPHTASE.

REPTO; ROWOTO00; PRITYHPHTASE.

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PROTEIN-TYROSINE PHOSPHATASE.
PHOSPHOCYSTEINE INTERMEDIATE (BY
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PROTEIN-TYROSINE PHOSPHATASE
EXTRACELLULAR (POTENTIAL).
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FIBRONECTIN TYPE-III 1.
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use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See h or send an email to license@isb-sib.ch).
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EMBL; D37781; BAA07035.1; -
EMBL; AP387824; AAM69432.1; JOINED.
EMBL; AP387824; AAM69432.1; JOINED.
EMBL; AP387824; AAM69432.1; JOINED.
EMBL; AP387825; AAM69432.1; JOINED.
EMBL; AP387826; AAM69432.1; JOINED.
EMBL; AP387829; AAM69432.1; JOINED.
EMBL; AP387829; AAM69432.1; JOINED.
EMBL; AP387831; AAM69432.1; JOINED.
EMBL; AP387831; AAM69432.1; JOINED.
EMBL; AP387834; AAM69432.1; JOINED.
EMBL; AP387835; AAM69432.1; JOINED.
EMBL; AP387835; AAM69432.1; JOINED.
EMBL; AP387836; AAM69432.1; JOINED.
EMBL; AP387839; AAM69432.1; JOINED.
EMBL; AP387839; AAM69432.1; JOINED.
EMBL; AP387839; AAM69432.1; JOINED.
EMBL; AP387839; AAM69432.1; JOINED.
EMBL; AP387841; AAM69432.1; JOINED.
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PTPG HUMAN STANDARD; PRT; 1445 AA.
P23470; Q15623;
Q15623;
Q1-NOV-1991 (Rel. 20, Created)
Q1-PEB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
gamma precein-tyrosine phosphatase gamma precursor (BC 3.1.3.48) (R-PTP-PTPRG.
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EXTRACELLULAR (POTENTIAL).
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FIBRONECTIN TYPE-III.
PROTEIN-TYROSINE PHOSPHATASE 1.
PROTEIN-TYROSINE PHOSPHATASE 2.
PROTEIN-TYROSINE PHOSPHATASE 2.
PHOSPHOCYSTEINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                                                                                           EMBL, L09562; AAA40022.1; -
EMBL, L09562; AAA40022.1; -
EMBL, L09562; AAA40022.1; -
EMBSP, PB652; 1YPO.
EMBC, MI19764; Ptpg.
MGD; MG19764; Ptpg.
EmerPro; IPR00148; Euk Coanhd.
EmerPro; IPR00148; Euk MIII.
EmerPro; IPR0003961; TYR_phosphatase.
EmerPro; IPR000342; TYR_phosphatase.
Emis PP00141; fil3; -
Emis PP00141; fil3; -
Emis PP00102; PR00700; PRTYPHPHTASE.
Emis PP00102; PR00700; PRTYPHPHTASE.
Emis PP00103; TYR_PHOSPHATASE 1; 1.
Emis PEOSITE; PS000383; TYR_PHOSPHATASE 1; 1.
Emcorra; PS000383; TYR_PHOSPHATASE 1; 1.
Emcorra;
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Best Local Similarity
Matches 12; Conserv
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-!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
-!- TISSUB SPECIFICITY: Detected in brain, lung, kidney, heart, liver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VAR_015906.
61 G -> D (IN REF. 1).
29 YNGYLEPLGSYR -> LQWEAGTSGLLP (IN REF. 2)
145926 MW; E6752D521C4B6AFE CRC64;
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1-FBB-1994 (Rel. 28, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Protein-tyrosine phosphatase gamma precursor (EC 3.1.3.48) (R-PTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxIb=10090;
                                   (POTENTIAL)
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Q -> P (in colon cancer, somatic mutation).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 87:7000-7004 (1990).

-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.

-!- Tyrosine + phosphate.

-!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).

-!- TISSUB SPECIFICITY: Found in a variety of tissues. It is developmentally regulated in the brain (By simlarity).

-!- SIMILARITY: Contains I eukaryotic-type carbonic anhydrase domain.

-!- SIMILARITY: Contains 1 protein-tyrosine phosphatase domains.

-!- SIMILARITY: Contains 1 fibronectin type III domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Brain;
MEDIARE-90384936; PubMed=2169617;
Kaplan R., Morse B., Huebner K., Croce C., Howk R., Ravera M.,
Ricca G., Jaye M., Schlessinger J.;
"Cloning of three human tyrosine phosphatases reveals a multigene family of receptor-linked protein-tyrosine-phosphatases expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Krueger N.X., Streuli M., Saito H.,
"Structural diversity and evolution of human receptor-like protein
tyrosine phosphatases.";
                                                                                   SEQUENCE FROM N.A.

MEDIJNE=93180796; PubMed=8382771;

MEDIJNE=93180796; PubMed=8382771;

Barnea G., Silvennoinen O., Shaanan B., Honegger A.M., Canoll P.D., Bustachio P., Morse B., Levy J.B., Laforgia S., Huebner K., Musacchio J.M., Sap J., Schlessinger J.;

"Identification of a carbonic anhydrase-like domain in the "receptor tyrosine phosphatases.";

Mol. Cell. Biol. 13:1497-1506(1993).
                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                             MEDIINE-56429999; PubMed-88331499; Kastury K., Ohta M., Lasota J., Moir D., Dorman T., Laforgia S., Druck T., Huebner K.; R. "Structure of the human receptor tyrosine phosphatase gamma gene (PTPRG) and relation to the familial RCC t (3,8) chromosome
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AACS0439.1; JOINED.
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AACS0439.1; JOINED.
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   Homo sapiens (Human).
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                     NCBI_TaxID=9606;
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REMEL; U46102; AACS0439.1; JOINED.
REMEL; U46102; AACS0439.1; JOINED.
REMEL; U46104; AACS0439.1; JOINED.
REMEL; U46104; AACS0439.1; JOINED.
REMEL; U46105; AACS0439.1; JOINED.
REMEL; U46105; AACS0439.1; JOINED.
REMEL; U46110; AACS0439.1; JOINED.
REMEL; U46110; AACS0439.1; JOINED.
REMEL; U46110; AACS0439.1; JOINED.
REMEL; U461110; AACS0439.1; JOINED.
REMEL; U46110; REMEMER; REMORA, TAYER, REMORA, TAYER, SENOOS, TAYERHERMARS.
REMEL; REMORA, TEMPOREMARAS.
REMEL; REMER; REMORAN.
REMEL; REMER; REM
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92 92 Y -> H (IN REF. 2).

549 549 A -> V (IN REF. 2).

756 756 I -> T (IN REF. 2).

1407 1407 R -> M (IN REF. 3).

1445 AA; 162058 MW; 350FB90DC94R808D CRC64;
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CARBONIC-ANHYDRASE LIKE.
PIBRONECTIN TYPE-III.
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N-LINKED (GLCNAC...)

N-LINKED (GLCNAC...)
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                                                                                                                                                      01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
10-CTT-2003 (Rel. 42, Last annotation update)
10-CTT-consine phosphatase DPTP precursor (EC 3.1.3.48) (Protein-tyrosine-phosphate phosphohydrolase).
                                                                                                                                                                                                                                                                                                                                   PROTEIN-TYROSINE PHOSPHATASE DPTP.
                                                                                     Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endoptera; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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IG-LIKE C2-TYPE 1.
                               PRT; 1462 AA
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                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=90046860; PubMed=2554325
                                                                                                                                                                                                                                                                                                               EMBL, M27699, AAA28842.1; -. PIR, B36182, B36182.
HSSP, P18052; IYFO.
                               STANDARD;
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15-JUL-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 4). Last annotation update)
15-MAR-2004 (Rel. 4). Last annotation update)
(Receptor-type protein-tyrosine phosphatase V precursor (BC 3.1.3.48)
(Embryonic stem cell protein-tyrosine phosphatase) (BS cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
VCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee K., Nichols J., Smith A.;
Mech. Dev. 61:213-215(1996).
-!- FUNCTION: May play a role in the maintenance of pluripotency.
Down-regulated during differentiation.
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(POTENTIAL)
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MEDLINE=97109513; PubMed=8951793;
Lee K., Nichols J., Smith A.;
"Identification of a developmentally regulated protein tyrosine phosphatase in embryonic stem cells that is a marker of pluripotential epiblast and early mesoderm.";
Mech. Dev. 59:153-164(1996).
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FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
PROTEIN-TYROSINE PHOSPHATASE 1.
PROTEIN-TYROSINE PHOSPHATASE 2.
PHOSPHOCYSTEINE INTERMEDIATE (BY
SIMILARITY).
                                                                                                               PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).
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                         tyrosine + phosphate.
SUBCELULLAR LOCATION: Type I membrane protein.
DEVELOPMENTAL STAGE: Detectable in the epiblast of oocytes and throughout early mouse embryo development. In adult, expression is localized in gonadal germ cells.
SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
SIMILARITY: Contains 10 fibronectin type III domains.
CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
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PROTEIN-TYROSINE PHOSPHATASE 2.
PHOSPHOCYSTEINE INTERMEDIATE (BY
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R HSCP; P18052; 1YFO.
R MGD; MGI.108027; PFDY.
InterPro; IPR003957; FN III-like.
R InterPro; IPR003957; FN III-like.
R InterPro; IPR003967; TYF phosphatase.
R InterPro; IPR001242; TYF PP.
R Pfam; PF001021; Yahosphatase; 1.
R Pfam; PF00102; Yahosphatase; 1.
R PKINTS; PR00100; PTPC; 1.
R PKINTS; PR00100; PTPC; 1.
R PROSITE; PS00383; TYR PHOSPHATASE 1; 1.
R PROSITE; PS00383; TYR PHOSPHATASE 2; 1.
R PROSITE; PS00365; TYR PHOSPHATASE 3; 1.
R PROSITE; PS00365; TYR 
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FIBRONECTIN TYPE-III 1.
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Note=No experimental confirmation available;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Bone and testis. In the latter, restricted to
the basal portion of the seminiferous tubule.
DEVELOPMENTAL STACE: Up-regulated in differentiating cultures of
primary osteoblasts and down-regulated in late stage mineralizing
cultures. In testis, expression is highest between stages i and
VII when maturing spermatids remain buried within the sertoli
                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Receptor-type protein-tyrosine phosphatase V precursor (EC 3.1.3.48)
(Embryonic stem cell protein-tyrosine phosphatase) (ES cell
phosphatase) (Osteotesticular protein-tyrosine phosphatase) (CST-PTP)
PTPRV OR ESP.
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
Comment=A presumed alternate transcript of 4.8-5.0 kilobases,
which may lack PTP domains, is present in proliferating
osteoblasts, but not detectable at other stages;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDUCTION: By parathyroid hormone and cAMP analogs. PTM: The cytoplasmic domain contains potential phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-95074080; PubMed=7527035;
Mauro L.J., Olmsted B.A., Skrobacz B.M., Mourey R.J., Davis A.R.,
Dixon J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Contains 2 protein-tyrosine phosphatase domains. SIMILARITY: Contains 10 fibronectin type III domains.
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Length 1705;
                                  Indels
   DB 1; L
                                                                                                                                                                                       PRT; 1711 AA.
2.8%; ....
100.0%; Pred. No. ...
0; Mismatches
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                                                                                            1347 LVHCSAGVGRTG 1358
                                                                     356 LVHCSAGVGRTG 367
 Query Match 2.8
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FISSUE=Osteosarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
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                                                                                                                                                                                         PTPV RAT
064612;
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RECEPTOR-TYPE PROTEIN-TYROSINE
RECEPTOR-TYPE PROTEIN-TYROSINE
POTENTIAL.
CYTOPLARIC (POTENTIAL).
CYTOPLARIC (POTENTIAL).
CYTOPLARIC (POTENTIAL).
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 7.
FIBRONECTIN TYPE-III 9.
FIBRONECTIN TYPE-III 9.
FIBRONECTIN TYPE-III 9.
FIBRONECTIN TYPE-III 19.
FIBRONECTIN 
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             HSSP, P18052, PARCOSTILL, P.
HSSP, P18052, P180624, PTF0.
InterPro; IPR000897; FN III-like.
InterPro; IPR000387; TYT phosphatase.
InterPro; IPR000242; TYT phosphatase.
InterPro; IPR000242; TYT phosphatase.
PEAM, PF00102, Y phosphatase.
PRINTS, PR00104; FPF2, PPF2, PRNO1060; PTTPHPHTASE.
SMATY, SM00060; FN3, 8.
SMATY, SM00060; FN3, 8.
SMATY, SM0018; PTF2, IVE PHOSPHATASE 1; 1.
PROSITE; PS50056; TYT PHOSPHATASE 2; 1.
PROSITE; PS50056; TYT PHOSPHATASE PTP, 2.
Hydrolase; Transmembrane; Repeat, Signal, Glycoprotein; Alternative splicing.
SIGNAL 18 1711 RECEPTOR-TYPE PROSINE.
CHAIN 18 1711 RECEPTOR-TYPE PROFIN-
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1711 AA;
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ö Query Match 2.8%; Score 12; DB 1; Length 1711; Best Local Similarity 100.0%; Pred. No. 0.00077; Matches 12; Conservative 0; Mismatches 0; Indels

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Gaps

356 LVHCSAGVGRTG 367 |||||||||||| 1347 LVHCSAGVGRTG 1358

sarch completed: June 16, 2004, 13:31:59
bb time : 18 secs

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Q9iba0 potamotrygo Q9yjb brachydanio Q64696 mus musculu Q9iai8 xenopus lae Q81169 mus musculu Q90yj4 brachydanio Q723x4 homo sapien Q1723x musculu Q96bb0 mus musculu Q96bb0 mus musculu Q96bb0 mus musculu Q7500 homo, sapien
                                                                                                                                    090015 gallus gall
090005 gallus gall
09000 rattus sp.
07t17 mus masculu
09um81 homo sapien
09iaj veropus lae
054605 rattus sp.
09qw67 rattus sp.
09dw87 rattus sp.
09dw87 rattus sp.
09dw87 rattus sp.
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Q64604 r protein-t
Q64609 mus musculu
Q44328 hirudo medi
Q88488 rattus norv
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O9n108 eptatretus
O9jlj6 mus musculu
O02048 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Obsugi M., Kuramochi S., Matsuda S., Yamamoto T., "Molecular cloning and characterization of a novel cytoplasmic protein-tyrosine phosphatase that is specifically expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    December
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Protein-tyrosine-phosphatase (EC 3.1.3.48).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       426 AA
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J. Biol. Chem. 272:33092-33099(1997).
                Q90YJ5
Q64696
Q9IAI8
Q8R169
Q90YJ4
Q7Z3X4
Q17024
Q8VBV0
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01-JUN-1998 (TrEMBLrel. 06, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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Q9LAJO
Q64665
Q9QM67
Q64487
Q9LAJI
Q9EQ17
Q9EQ17
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Q9QW00
Q7TT17
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MEDLINE=98070510; PubMed=9407093;
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Q9y406 homo sapien
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                                                                                                June 16, 2004, 13:28:47; Search time 45 Seconds
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                 GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Query Match
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01-NOV-1999 (TrEMBLrel, 12, Created)
01-NOV-1999 (TrEMBLrel, 12, Last sequence update)
01-UNOV-2003 (TrEMBLrel, 24, Last annotation update)
Hypotherical protein (Fragment).
DYF2P566K0524.
DYF2P566K0524.
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL: AL050040; CAB43248.1; -.

PIR: T08716; T08716.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0004705; F:protein emino acid dephospharase activity; IEA.

GO; GO:00064705; P:protein amino acid dephosphorylation; IEA.

InterPro; IPR000281; TYR_phospharase.
                                                                                                                                                                                                                                                                                 Length 426;
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Local Similarity 100.0%; Pred. No. 0;
tes 426; Conservative 0; Mismatches
InterPro; IPR000242; Tyr_PP.
PRIM: PRO00102; Tyr_PP.
PRINTS; PR007100; PRTYPHPHTASE.
SWART; SM00194; PTPC; 1.
PROSITE; PS001383 TYR_PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE 2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE 2; 1.
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Matches 426, Conservative
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421 NLLALY 426
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TISSUE=Kidney;
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SEQUENCE
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                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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EMBL, D83072; BAA19740.1; -.

HASP, P29150; 1GWZ.

MGD; MGI:1344406; Ptpn21.

GO; GO:00167187; F:hydrolase activity; IEA.

GO; GO:00167187; F:hydrolase activity; IEA.

GO; GO:0004725; F:protein tyrosine phosphatuse activity; IEA.

GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.5%; Score 15; DB 11; Length 336; 100.0%; Pred. No. 5.1e-07; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                    Length 398;
                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=CS7-BL6; TISSUB=Testis;
Niehiyama H., Higashitsuji H., Fujita J.;
"Expression of mouse PTP-RLIO isoforms in testis.";
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 336 AA; 38503 MW; 679B683660C39FFD CRC64;
                                                                                                                                                                                                                 SEQUENCE 398 AA; 45690 MW; 857AAD03747870A2 CRC64;
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Last annotation update)
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Last sequence update)
Last annotation update)
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Local Similarity 100.0%; Pred. No. 2.9e-11;
les 19; Conservative 0; Mismatches 0;
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InterPro; 1PR000242; TYR phosphatase.
InterPro; 1PR000242; TYR PP.
PRam; PR00102; Y_phosphatase; 1.
PRAMT; SM00194; PTPC; 1.
PROSITE; PS000383; TYR PHOSPHATASE 1; 1.
PROSITE; PS000383; TYR PHOSPHATASE 2; 1.
PROSITE; PS00058; TYR PHOSPHATASE 2; 1.
REMINES, PROOFOO, PRIVEHENTASE.
SMART, SWOO194, PIPC, 1.
PROSITE, PSOO383, TYR_PHOSPHATASE_1; 1.
PROSITE; PSSOO56; TYR_PHOSPHATASE_1; 1.
PROSITE; PSSOO56; TYR_PHOSPHATASE_1; 1.
PROSITE; PSSOO56; TYR_PHOSPHATASE_PIP; 1.
HYPOTHERICAL PROCEEN: Hydrolase.
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G9Y1X4;

G9Y1X4;

01-NOV-1999 (TEMBLrel. 12, Last seq

01-NOV-1999 (TEMBLrel. 12, Last seq

01-NOV-1999 (TEMBLrel. 24, Last ann

SPTPR5 (Fragment).

Bphydatia fluviatilis.
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                                                                                                                                                                                                                                                                                                                                                                                                           164 KNRYRDILPYDSTRVPLGK 182
                                                                                                                                                                                                                                                                                                                                                                                 192 KNRYRDILPYDSTRVPLGK 210
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MCBI_TaxID=9606;
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088571
ID 088571 PI
AC 088571;
DT 01-NOV-1998 ('DT 01-NOV-1998 ('DT)
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SEQUENCE FROM N.A.

STAIN-CZECH II; TISSUE-Breast tumor;

STAIN-CZECH II; TISSUE-Breast tumor;

STRAIN-CZECH II; TISSUE-Breast tumor;

Strausberg R.L., Feingold E.A., Grouse i.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse i.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner I., Shemmen C.M., Schuler G.D.,

Altschul S.F., Joedan H., Moore T., Max S.I., Wang J., Hale F.,

Diatchenko L., Marusina K., Parmer A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Ubdin T.B., Toshiyvixi S., Carninol P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., NcKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Fale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences:";

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences:";
                                                                                                                                              MEDLINE=99246376; PubMed=10229569; Miyata T.; ODOO K., Suga H., Iwabe N., Kuma K., Miyata T.; Multiple protein tyrosine phosphatases in sponges and explosive gene duplication in the early evolution of animals before the parazoan-eumetazoan split.";
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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01-0CT-2003 (TrEMBirel. 25, Last sequence update)
01-0CT-2003 (TrEMBirel. 25, Last annotation update)
Protein tyrosine phosphatase, non-receptor type 21 (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO: GO:0016787; F:hydrolase activity; IEA.
GO: GO:0004725; F:hydrolase activity; IEA.
GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
GO: GO:0004705; P:protein amino acid dephosphorylation; IEA.
InterPro: IRR00387; TYR Phosphatase.
InterPro: IRR00387; TYR PP.
FEAM: PF00102; Y phosphatase.
FRINTS; PR00700; PRTYPHHTASE.
SWART; SW00104; PTPC; 2.
PROSITE: PS000383; TYR PHOSPHATASE 1; 1.
PROSITE: PS500056; TYR PHOSPHATASE 2; 2.
PROSITE: PS500055; TYR PHOSPHATASE 2; 2.
Eukaryota, Metazoa, Porifera, Demospongiae, Ceractinomorpha,
Haplosclerida, Spongillidae, Ephydatia.
MCBI_TaxID=31330,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.5%; Score 15; DB 5; Length 446; Best Local Similarity 100.0%; Pred. No. 6.6e-07; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 446 AA; 50365 MW; 9E5B8AF6168FDF7C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                       J. MOI. BVOI. 48:654-662(1999).
EMBL, AB019127; BAA82560.1; -.
HSSP; P18052; 1YFO.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
011175B15.2 (Protein tyrosine phosphatase, non-receptor type 21)
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                                                                                                                                                                                  DB 11; Length 758;
1.1e-06;
hes 0; Indels
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3.5%; Score 15; DB 4; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homosapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelo
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                                                     1024 AA; 115763 MW; C702F90D6AF38EAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Howden P.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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(TrEMBLrel. 08, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1024 AA
                                                                                                                                                                                  Query Match 3.5%; Score 15; DB Best Local Similarity 100.0%; Pred. No. 1.1 Matches 15; Conservative 0; Mismatches
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PROSITE; PS00057; FERM 3; 1.

PROSITE; PS00033; TYR PHOSPHATASE 1; 1.

PROSITE; PS50056; TYR PHOSPHATASE 2; 1.

PROSITE; PS50055; TYR PHOSPHATASE PTP; 1.
[2]
SEQUENCE PROM N.A.
STRAIN-CZECH II; TISSUE-Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                354 PLLVHCSAGVGRTGV 368
                                                                                                                                                                                                                                                                                      687 PLLVHCSAGVGRTGV 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354 PLLVHCSAGVGRTGV 368
                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Best Local Similarity
Matches 14; Conserv
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SEQUENCE
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MEDIANE=8839510.0; PubMed=9727007;
Wright Wn.B., Hugo C., Seifert R., Disteche C.M., Bowen-Pope D.F.;
Wright Wn.B., Hugo C., Seifert R., Disteche C.M., Bowen-Pope D.F.;
Wright Wn.B., Hugo C., Seifert R., Disteche C.M., Bowen-Pope D.F.;
Wright Wn.B., Hugo C., Seifert R., Disteche C.M., Bowen-Pope D.F.;
Wright Wn.B., Hugo C., Seifert R., Disterning to injury express a novel receptor protein-tyrosine phosphatase in experimental mesangial proliferative glomerulonephritis.";
J. Biol. Chem. 273:3929-2393(1998).

EMBL, AF073999, AAC34823.1;
MGD, MGI:1096349, Prpred
GO: GO:0004721; F:pydrolase activity; IEA.
GO: GO:0004721; F:pydrolase activity; IEA.
GO: GO:0004721; F:pydrolase activity; IEA.
GO: GO:0006470; P:pyrotein phosphatase.
GO: GO:0006470; P:pyrotein mino acid dephosphorylation; IEA.
FROSITE; PSG00383; TYR PHOSPHATASE 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Proliferating and migrating mesangial cells responding to injury express a novel receptor protein-tyrosine phosphatase in experimental mesangial proliferative glomerulonephritis.";

M. Biol. Chem. 273:23929-23937(1998).

BMBL; AF073998; AAC34822.1; -.
MGD; MGI:1096349; Prprq.

GO; GO:0016787; Frhydrolase activity; IEA.

GO; GO:0016787; Frhydrolase activity; IEA.

GO; GO:0004721; Frprotein phosphatase activity; IEA.

GO; GO:0006470; Protein amino acid dephosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                  Mus. Spretus (Western wild mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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MEDLINE=98395110; PubMed=9727007;
Wright M.B., Hugo C., Seifert R., Disteche C.M., Bowen-Pope D.F.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 24 AA; 2483 MW; 7E81ASFBF2BC2E2B CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
Protein tyrosine phosphatase rPTP-GMC1 (Fragment).
01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Protein tyrosine phosphatase rPTP-GMC1 (Fragment).
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v 100.0%; Pred. No. ...
o; Mismatches
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PROSITE, PS00383; TYR PHOSPHATASE 1; 1.
PROSITE, PS50056; TYR PHOSPHATASE 2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VHCSAGVGRTGVFI 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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SEQUENCE
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Best Local S
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CSTRAIN=CSTBL/GS, N.4.

SEGURANE FROM N.4.

KEDINE=22354683; PubMed=12466851;

A The FANTON Consortium,

The FANTON Consortium,

The RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

Mature 420:563-573 (2002)

REMBL; AK034667; BAC28569.1; -.

ROG) GO:00064705; Protein tyrosine phosphatase activity; IRA.

GO; GO:00064705; Protein amino acid dephosphorylation; IRA.

InterPro; IPR000359; PTPC_motif.

RITHERPRO; IPR003595; PTPC_motif.

RITHERPRO; IPR003595; PTPC_motif.

RITHERPRO; PR000003; Typhosphatase.

REMBL; PR001001; Typhosphatase.

REMBL; PR001001; PRTYPHPFFASE.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
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                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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Last annotation update)
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100.0%; Pred. No. 1.6e-06;
ive 0; Mismatches 0;
                       Pred. No. 5.3e-07;
                                                Wismatches
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PROSITE; PS50056; TYR PHOSPHATASE 2; 1.
PROSITE; PS50055; TYR PHOSPHATASE PTP; 1.
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100.08;
                                                                                                                                                                                                                                                                                  Q8CC23;
01-MAR-2003 (TrEMBLArel. 23, C;
01-MAR-2003 (TrEMBLArel. 23, L;
01-0CT-2003 (TrEMBLArel. 25, L;
UNKnOWN EST (Fragment).
PTPRD.
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01-MAR-2003 (TEMBLrel. 23,
01-MAR-2003 (TEMBLrel. 23,
^1-OCT-2003 (TEMBLrel. 25,
                                                                                            357 VHCSAGVGRTGVFI 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00404; PTPc motif;
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                                                                                                                                          10 VHCSAGVGRTGVFI 23
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                                                Conservative
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Query Match
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Q8C922,
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                                                                                               RESULT 12
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the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.";
Nature 420:563-573 (2002).
EMBL; AK033873; BAC28503.1; -.
MGD; MGT:97812; Prprd.
MGC:97812; Prprotein tyrosine phosphatase activity; IEA.
GO; GO:0004725; Prprotein tyrosine phosphatase activity; IEA.
GO; GO:0004725; Prprotein tyrosine phosphatase activity; IEA.
InterPro; IRR003895; Prpc motif.
InterPro; IRR003895; Prpc motif.
InterPro; IRR003842; Tyr Phosphatase.
Pfam; PF00102; Y_phosphatase; 1.
PRINTS; PR00700; PRTYPHPHASE.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
ACBI_TaxID=9606;
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Dayton M.A., Blanchard K.L.;

Dayton M.A., Blanchard K.L.;

"Differential expression of PTPage RNAs resulting from K562

differentiation induced by PRA.";

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; API69351; AAD50277.1;

HSSP, P18052; 1YFO.

GO; GO:0006470; P: hydrolase activity; IEA.

GO; GO:0006470; P: protein tyrosine phosphatase activity; IEA.

GO; GO:0006470; P: protein amino acid dephosphorylation; IEA.

InterPro; IRR000387; TYR_POSPhatase.

InterPro; IRR000387; TYR_PEP.

Pfam, PF00102; Y.phosphatase; 1.

PRINTS: PR007000; PRTYPHPHTASE.
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3.3%; Score 14; DB 4; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 AA; 10642 MW; 1BCCF472432BA0CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Protein tyrosine phosphatase RQ (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 AA
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PROSITE: PS00383; TYR_PHOSPHATASE 1; 1.
PROSITE: PS50056; TYR_PHOSPHATASE 2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE PTP; 1.
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PROSITE; PS00383; TYR PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR PHOSPHATASE 2; 1.
PROSITE; PS50055; TYR PHOSPHATASE PIP; 1.
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NON TER
NON TER
SEQUENCE
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SEQUENCE
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Best Local S:
Matches 14
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99 VHCSAGVGRTGVFI 112

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-2257BL/63; TISSUE-Cerebellum;
MEDLINE-22354633; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I will Team;
whale place the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.";
Nature 420:563-573(2002).
EMBL; ASK042201; BAC3488.1; -.
GG), GO:0004725; F:protein tyrosine phosphatase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (1]—SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDIJNE=9246376; PubMed=10229569;
ONO K., Suga H., Iwabe N., Kuma K., Miyata T.;
"Multiple protein tyrosine phosphatases in sponges and explosive gene duplication in the early evolution of animals before the parazoan-eumetazoan split.";
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentía; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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R GO; GO:0016725; F:protein tyrosine phosphatase activity; IEA.
R GO; GO:0006470; F:protein tyrosine phosphatase activity; IEA.
R GO; GO:0006470; F:protein amino acid dephosphorylation; IEA.
R InterPro; IPR000387; TYR phosphatase.
R InterPro; IPR000387; TYR phosphatase.
R PARNY; PR00100; PRTYPHPHTASE.
R PRINT; SM00194; PTPC.
R PROSITE; PS00383; TYR PHOSPHATASE 1; 1.
R PROSITE; PS00365; TYR PHOSPHATASE 2; 1.
R PROSITE; PS0056; TYR PHOSPHATASE 2; 1.
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100.0%; Pred. No. 3.4e-06;
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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EMBL; AB019128; BAA82561.1; -.
HSSP; P18052; IYFO.
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01-MAR-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
Unknown EST (Fragment).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Sprague Dawley; TISSUE-Brain;
MEDLINE-94075340; PubMed-8253779;
Longo F.M., Martignetti J.A., Le Beau J.M., Zhang J.S., Barnes J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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J. Biol. Chem. 268:26503-26511(1993).
EMBL; U00477; AAC04306.1; -.
PIR; A56493; A56493.
HSSP; P18052; 17FO.
GO; GO:0016797; F:hydrolase activity; IEA.
GO; GO:0016797; F:hydrolase activity; IEA.
GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
GO; GO:0004725; F:receptor activity; IEA.
FPRODIO22; T:RE-PHOSPHATASE.
SMRAT; SM00194; PPRC; 2.
PRINTS; PROO700; PRITYPHPHTASE.
SMRAT; SM00194; PPRC; 2.
PROSITE; PSS0056; TYR_PHOSPHATASE_2; 2.
PROSITE; PSS0056; TYR_PHOSPHATASE_2; 2.
HYDROSITE; PSS0055; TYR_PHOSPHATASE_2; 2.
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GO:0006470; P:protein amino acid dephosphorylation; IEA.
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Pred. No. 3.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.3%; Score 14; DB 11; Length 460;
100.0%; Pred, No. 8.1e-06;
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SEQUENCE 192 AA; 22551 MW; B78B194500F33BIA CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                             InterPro; IPR003595; PTPC_motif.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; TYR_PP.
Ffam: PF00102; Y_phosphatase; I.
PRINTS; PR00700; PRTYPHPHTASE.
SMART; SM00194; PTPC: 1.
SMART; SM00404; PTPC: 1.
PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE 2; I.
NON TER.
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3.3%; Score 14; DB
Best Local Similarity 100.0%; Pred. No. 3.6
Matches 14; Conservative 0; Mismatches
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SEQUENCE 460 AA; 5
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les 14; Conserv
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MEDLINE=20219325, PubMed=10754074;
MEDLINE=20219325, PubMed=10754074;
MOD-Koyanagi K., Suga H., Katoh K., Miyata T.;
"Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
divergence of tissue-specific isoform genes in the early evolution of
                                                                                                                                                                                                                                                                                                                                                                    Potamotrygon motoro (South American freshwater stingray).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;

Myliobatiformes; Myliobatoidei; Potamotrygonidae; Potamotrygon.
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Pred. No. 8.2e-06;
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OJIBAS.

OLOCT-2000 (TrEMBLrel. 15, Created)

OLOCT-2000 (TrEMBLrel. 15, Last sequence update)

OLOCT-2003 (TrEMBLrel. 24, Last annotation update)

RyPTRP2AA.

RYPTRP2AA.
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Job time : 46 secs
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1586107 segs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 arched:

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SUMMARIES	ŗ	F.D.	AAW89249	AAW89250	AAW89251	AAE14454	ADE08106	AAE37996	ABG30845	ADD89795	ADE09123	ABG06042	AAE37994	AAG67637	AAG67458	ABU70688	AAR71498	AAW75999	AAY90272	AAB19343	AAW89252	AAW12522	AAY25156	AAG79333	ADD22982	ADD18742	ADE57117
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ALIGNMENTS

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PTF04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease; Hunfingron's disease.
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                                             AAW89249 standard; protein; 426
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                                                                                                                                                           10-MAR-1999
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RESULT 1
                            AAW89249
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98WO-US008439 WO9849317-A2. 27-APR-1998; 05-NOV-1998. Mus sp.

97US-0044428P. 97US-0047222P. 97US-0049477P. 97US-0049756P. 97US-0049914P. (SUGE-) SUGEN INC. 28-APR-1997; 20-MAY-1997; 11-JUN-1997; 11-JUN-1997; 23-OCT-1997;

Markby Onrust 5, Peles E, Jallal B, , Hui TH; Plowman GD, Clary D, J Courtneidge SA, App H, WPI; 1999-009434/01. N-PSDB; AAV81744.

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New mucleic acid encoding specific protein tyrosine phosphatases - useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease. Claim 2; Page 155-157; 193pp; English.

The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The present sequence represents mouse PTP05. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify

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substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. lenkaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor partincularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA, to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the
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100.0%; Pred. No. 2e-204;
ive 0; Mismatches 0;
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The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The presents equence represents mouse PTP05. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polymucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the

rotein tyrosine phosphatases - refor treatment and prevention of

New nucleic acid encoding specific protein tyrosine for identifying specific modulators for treatment an cancer and neurodegenerative disease.

Claim 2; Page 157-158; 193pp; English

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Markby

Onrust S,

щ Peles

Jallal B, Hui TH;

Courtneidge SA, App H,

WPI; 1999-009434/01.

N-PSDB; AAV81745

Clary D,

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Plowman

INC.

(SUGE-) SUGEN

18-JUN-1997; 23-OCT-1997;

97US-0047222P. 97US-0049477P. 97US-0049756P. 97US-0049914P. 97US-0063595P.

97US-0044428P

28-APR-1997 20-MAY-1997 11-JUN-1997 11-JUN-1997

98WO-US008439

27-APR-1998;

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DVSDRSIRNRWNSMDSETAGPSKTVSPVLSGSSRLSKDTETSVSEKELTQLAQIRPLIFN 180
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                                                                 MSSPRKVRGKTGRDNDEEEGNSGNLNLRNSLPSSSQKMTPTKP-
 Score 2212.5; DB 2
Pred. No. 1.2e-201;
0; Mismatches 0;
tch 98.7%; al Similarity 92.0%; 426; Conservative
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Mouse PTP05 isoform #1

WO9849317-A2

Mus sp

05-NOV-1998

(first

10-MAR-1999

AAW89250;

ESULT 2 AW89250

300

323 360 383 420

FIKWDDHGTPASADFFIKKVRYVRXSHITGPLLVHCSAGVGRIGVFICVDVVFSAIEKNY

361

203 240 263

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37;

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Sequence 463 AA;

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m

SFDIMNIVTOMRKQRCGMIQTKEQYQFCYBIVLEVLQNLLALY 463

protein; 405 AA

AAW89251 standard;

SSULT 3

(first entry)

10-MAR-1999

AAW89251;

Mouse PTP05 isoform #2.

SPDIMNIVPOMRKQRCGMIQTKBQYQFCYRIVLAVLQNLLALY

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                                                    SFSDKYELVYPEPLESDTDETVWDVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSK
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/note= "Tyrosine specific protein phosphatase active
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/note= "Protein-tyrosine phosphatase"
340. .388
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/note= "Tyr_phosphatase"
362. .379
/label= Transmembrane_domain
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29-JUN-2000; 2000US-0215210P
06-JUL-2000; 2000US-021829P
12-JUL-2000; 2000US-0218080P
21-JUL-2000; 2000US-0220117P
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Onrust S,

Peles E,

Jallal B, , Hui TH;

Plowman GD, Clary D, J. Courtneidge SA, App H,

(SUGE-) SUGEN INC.

WPI; 1999-009434/01.

N-PSDB; AAV81746

97US-0044428P. 97US-0047222P. 97US-0049477P. 97US-0049756P. 97US-00435914P.

11-JUN-1997; 11-JUN-1997; 18-JUN-1997;

23-OCT-1997

98WO-US008439

27-APR-1998; 28-APR-1997

05-NOV-1998

WO9849317-A2

Mus

Claim 2; Page 158-160; 193pp; English. cancer and neurodegenerative disease.

95.2%; Score 2133; DB 2; Length 405; 100.0%; Pred. No. 3.7e-194; tive 0; Mismatches 0; Indels (

Best Local Similarity 100. Matches 405; Conservative

Query Match

Sequence 405 AA;

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Aur.Young J, Raughn MR, Ding L, Elliott VS, Gandhi AR, Griffin JA; Hafalia A, Kearney L, Lee EA, In Y, Mayan DB, Patterson C; Ramkunar J, Reddy R, Sanjarala MS, Stewart EA, Tang TY, Thornton M; Tribouley CM, Walia NK, Yang J, Yao MG, Yue H; Tribouley CM, Walia NK, Yang J, Yao MG, Yue H; Tribouley CM, Walia NK, Yang J, Yao MG, Yue H; Mankunar J, Rabozaca C, Majarana MS, Stewart EA, Tang TY, Thornton M; Movel polypeptide, useful for diagnosing, treating or preventing discretes of growth and development, immune system, neurological and cell proliferation discretes of growth and polypeptide are useful in the diagnosis, treatment and polypeptides.

Claim 1, Page 105-106; 115pp; English.

Crim present sequence is human protein phosphatase (PP) 4. PP polymicleotide and polypeptide are useful in the diagnosis, treatment and prevention of immune system disorders; neurological disorders. Stamples of celevolopmental disorders and cell proliferative diagnoders, retament and prevention of immune system disorders and cell proliferative diagnosis, treatment and prevention of stamps and cell proliferative diagnosis, retament and prevention of stamps and cell proliferative disorders and cell proliferative diagnosis, untiline cell cell of meunodeficiency disease, and include acquired immune deficiency grants and cell of ce
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Sequence 420 AA;

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7 240 ETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQ 299 SPSDKYELVYPEPLESDIDETVWDVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSK 120 DTBTSVSEKELTQLAQIRPLIFNSSARSAMRDCLWTLQKK-BELDIIRBFLE1EQMTLPD 179 DFNSGNTLQNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEBYFYIATQGPLP 239 233 234 STIDDFWQMVLENNSNVIAMITREIEGGIIKCYHYWPISLKKPLELKHFRVFLENYQILQ 293 300 YFTVRVPQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHC 359 9 9 1 MSSPRKVRGKTGRDNDEBEGNSGNLNLRNSLPSSSQKMTPTKPIFGNKMNSENVKPSHHL 1 MSSPRDFRAEPVNDYBGNDSEAEDLNFRETLPSSSQENTPRSKVFENKVNSEKVKLSLRN Gapa ώ DB 5; Length 420; 62.7%; Score 1406; DB 5; Length 4; 64.1%; Pred. No. 7.6e-125; Length 4: ive 53; Mismatches 92; Indels Query Match
Best Local Similarity 64.13
Matches 273; Conservative 121 61 180 174

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3 SPR--KVRGKTGRDNDEBEGNSGNINLRNSLPSSSQKMTPTKPIFGNKMNSENVKPSHHL

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4,
                                                              354 SAGIGRIGVPLCVDVVFCALVKNCSFNIMDIVAQMREQRSGMVQTKEQYHFCYDIVLEVL 413
294 YFIIRMFQVVEKSTGTSHSVKQLQFTKWPDHGTPASADSFIKYIRYARKSHLTGPMVVHC 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed, as molecular weight markers on gels, as chromosome markers or tags, to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang J;
Wang Z;
                                              SAGVGRIGVFICVDVVFSAIBKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYBIVLEVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides, useful for expressing recombinant proteins for
                                                                                                                                                                                                                                                                                                                            novel gene, novel protein; tissue marker; molecular weight marker; chromosome marker; genetic disorder.
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                                                                                                                                                                                                                                                                                                     Novel protein (useful for identifying genetic disorders) #261.
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ou P, Drmanac RT,
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ehrman T, Weng G, Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID NO 1172; 1177pp; English.
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ng D, Chen R, Xu C, Boyle BJ;
                                                                                                                                                                                                               ADE08106 standard; protein; 508 AA.
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; 2001US-0339453P.
; 2002US-0365991P.
; 2002US-0365384P.
; 2002US-0372381P.
; 2002US-0372615P.
; 2002US-0012858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-DEC-2002; 2002WO-US039555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT, Asundi V, Goodri
Ghosh M, Xue AJ, Wehrman
                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                         QNLLAL 425
                                                                                                                                      414 RKLLTL 419
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11-DEC-2001; 2
14-MAR-2002; 2
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12-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                             Unidentified.
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis; atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer; psoriasis; thromobocytopaenia; developmental disorder; Reiter's Saydarome; renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease hautoimmune disorder; parkinson's disease; epilepsy; glomerulonephritis; autoimmune disorder; parkinson's disease; epilepsy; glomerulonephritis; acquired immune deficiency syndrome; immunosuppressive; Crohn's disease; nootropic; transgenic; dermatitis; multiple sclerosis; diabetes mellitus; allergy; gout; Grave's disease; Mashimoto's thyroditis; bowel syndrome; osteoporosis; rheumatoid arthritis; Sjogren's syndrome; osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological; gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.
                                                                                                                                                                                                                               ETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                     YFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAGVGRICYPICVDVVFSAIBKNYSFDIMNIVTOMRKORCGMIQTKEOYOFCYBIVLEVL 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kable AE, Chien D, Wilson AD, Swarnakar A, Gorvad AE;
Hafalia AJA, Emerling BM, Ramkumar J, Jin P, Griffin JA, Marquis JP;
Baughn MR, Chawla NK, Lehr-Mason PM, Khare R, Lee S, Hawkins PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FPHNDYEDVFEBPSESGSDPSWWTARGPPRRDRWSSEDBBAAGDSQALSPLLS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human kinase and phosphatase (KPP-41) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-DEC-2001; 2001US-0340233P.
19-DEC-2001; 2001US-0343007P.
21-DEC-2001; 2001US-0343546P.
04-FEB-2002; 2002US-0354388P.
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AE37996
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The invention relates to an isolated polypeptide, which is a human kinase and phosphatase (KPP). KPP agonists and antagonists are useful for diagnosing, treating or preventing disorders associated with aberrant expression of KPP, particularly cell prodiferative disorders (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal nocturnal heamoglobinuria, polycytheemia vera, psoriasis, primary thrombocytopaenia or cancel, developmental disorders (e.g. rocturnal heamoglobinuria, polycythemia vera, psoriasis, primary thrombocytopaenia or mental retardation), neurological disorders (e.g. aridosis, andemna or mental retardation), neurological disorders (e.g. alizedies, asthma, autoimmune thyroiditis, contact dermatiis, Crohn's allergies, asthma, autoimmune thyroiditis, contact dermatiis, Crohn's disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, allergies, asthma, athemine thyroiditis, irritable bowel syndrome, gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome, multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral, betterial, fungal, parasitic, protozoan or helminthic infections. The KPP expression of nucleic acids and kinases and phosphatases. KPP gene is useful in gene therapy and for creating transgenic animals to model human kpp protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SFSDKYBLVYPEPLESDTDETVWDVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIETSVSEKELTQLAQIRPLIFNSSARSAMRDCLATLOKK-EELDIIREFLELEQMTLPD 179
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                                                                                                                           disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 YFIIRMFQVVEKSTGTSHSVKQLQFTKWPDHGTPA.SADSFIKYIRYARKSHLTGPMVVHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSSPRKVRGKTGRDNDEEEGNSGNINLRNSIPSSSOKWTPTKPIFGNKANSENVKPSHHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                   New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disor (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
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63.6%; Pred. No. 8.4e-118;
ive 51; Mismatches 89;
    Zebarjadian Y;
                                                                                                                                                                                                       Claim 1; Page 243-244; 282pp; English.
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    Sprague WW,
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Best Local Similarity 63.69
Matches 259; Conservative
                                                                                                                                                             cancer or hepatitis.
                                         WPI; 2003-532894/50.
Lee SY,
                                                              N-PSDB; AAD57368.
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  Becha SD,
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AC ABG3
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(first entry)

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New human tyrosine phosphatase polypeptide, the regulation of which is useful for treating obesity, diabetes, cardiovascular or central nervous system disorder, chronic obstructive pulmonary disease and cancer.
                                                                           Human; tyrosine phosphatase; obesity; diabetes; Parkinson's disease; central nervous system disorder; CNS; cardiovascular disorder; stroke; chronic obstructive pulmonary disease; cancer; multiple sclerosis; dlzheimer's disease; Humington's disease; congestive heart failure; myocardial infarction; chromosome 10.
                                               Human tyrosine phosphatase protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 25; Fig 2; 145pp; English
                                                                                                                                                                                                                                                                              27-NOV-2001; 2001WO-EP013794
                                                                                                                                                                                                                                                                                                             27-NOV-2000; 2000US-0252912P.
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                                                                                                                                                                                                                                                                                                                                           (FARE ) BAYER AG
                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABK89178
                                                                                                                                                                                                               WO200242435-A2
                                                                                                                                                                                 Homo sapiens.
               21-0CT-2002
                                                                                                                                                                                                                                              30-MAY-2002.
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09-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                               Delaney AD;
The present invention relates to a new human tyrosine phosphatase polypeptide. The invention is useful for the preparation of a medicament for modulating the activity of human tyrosine phosphatase in a disease such as obseity, diabetes, a central nervous system (CNS) disorder, chronic obstructive pulmonary disease, cardiovascular disorder or cancer. The invention is useful for treating a human tyrosine phosphatase dysfunction related disease, preferably the above mentioned diseases. The invention is useful for treating the above mentioned disorders, where the CNS disorder is selected from Parkinson's disease, and the stroke, Alzheimer's disease, and Huntington's disease, and the cardiovascular disorder is selected from congestive heart failure and myocardial infarction. The molecules of the invention are useful in susceptibility to disease and abnormalities related to the presence of mutations in the polymucleotide coding the polymention. The mutanity sequence represents the human tyrosine phosphatase protein #1 of the invention. The sequence is encoded by the human tyrosine phosphatase tyrosine phosphatase gene located on chromosome 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETAGPSKTVSPVLSGSSRLSKDTETSVSEKELTQLAQIRPLIFNSSARSAMRDCLNTLQK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 EAAGPSOALSPLLS-----DTRKIVSEGELDOLAOIRPLIFNFHEGTAIKDCLKILEE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 YIRIVNHEBEYFYIATQGPLPETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPIS 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTKPI PGNKMISENVKPSHHLSFSDKYELVYPEPLESDIDETVWDVSDRSLRNRMNSMDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K-EELDIIREFLELEGMTLPDDFNSGNTLQNRDKNRYRDILPYDSTRVPLGKNKDYINAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.5%; Score 1310; DB 5; Length 398; 65.4%; Pred. No. 9.9e-116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 398 AA;
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Matches
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The present invention describes an isolated cancer associated phosphatase nucleic acid. Also described: (1) a method of screening for biologically a method for the diagnosis of cancer associated phosphatese function, (2) a method for the diagnosis of cancer; (3) a method for inhibiting the growth of a cancer cell; (4) methods of screening for targets of a cancer transduction in cancer cell; (5) a compound (C) for the tradement of trumour; (6) a composition for the treatment of a tumour comprising a pharmaceutical cariter and (C); (7) methods for treating a tumour in a patient. A cancer associated phosphatase of the present invention has cytostatic, immunosuppressive,
191 YIRIVNCGEBYFYIATQGPLLSTIDDFWQMVLENNSNVIAMITREMEGGIIKCYHYWPIS 250
                                                                                                                                          311 FIKYIRYARKSHLTGPMVHCSAGIGRTGVPLCVDVVPCAIVKDCSFNIMDIVAQMREQR 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer associated phosphatase; enzyme; human; cancer; tumour; cytostatic; immunosuppressive; antidiabetic; neuroprotective; antidiabetic; neuroprotective; antidiabetic; antiproriatic; antiarteriosclectotic; antimifiammatory; vulnerary; gynaecological; antiangiogenic; hyperproliferative disease; autoimmune disease; diabetes mellitus; multiple sclerosis; arteumatoid arthritis; psoriasis; atherosclerosis; inflammation; scarring; endometriosis; anglogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acids encoding cancer associated phosphatases, useful as targets for screening pharmaceutical agents that inhibit the growth of tumor cells, or for diagnosing and treating cancer, inflammation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       visualising tumours in patients or diagnosing and treating cancer, e.g
                                    LKEPLEPEHPSVPLETFHVTQVFTVRVPQIVKKSTGKSQCVKHLQPTKNPDHGTPASADF
                                                            251 LKXPLELKHFRVFLENYOILQYFIIRMFQVVEKSTGTSHSVKQLQFTKWPDHGTPASADS
                                                                                                                    FIKYVRYVRKSHITGPLLVHCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antidiabetic, neuroprotective, antirheumalic, antiarthritic, antipresoriatic, antiarteriosclerotic, antiinflammatory, vulnerary, gymaecological and antiangiogenic activities. The cancer associated phosphatases and mucleic acids encoding the proteins are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human DKFZP566K0524 protein SBQ ID NO:10
                                                                                                                                                                                                     399 CGMIQTKEQYQFCYRIVLEVLQNLLAL 425
                                                                                                                                                                                                                        SGWVQTKEQYHFCYDIVLEVLRKLLTL 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 10; 63pp; English.
                                                                                                                                                                                                                                                                                                                                               Ā
                                                                                                                                                                                                                                                                                                                                             ADD89795 standard; protein; 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-MAR-2003; 2003WO-CA000393.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAR-2002; 2002US-0368859P.
                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-902934/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                                                      ADD89795;
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                                                                                                                                                                                                                                                                                                      RESULT 8
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pancreas, lung, ovarian, liver or colon cancer. The polypeptides and nucleic acids may also be used for treating hyperproliferative diseases, such as autoimmune disease, disbetes mellitus, multiple sclerosis, rheumatoid arthritis, psoriasis, atherosclerosis, inflammation, scarring, endometriosis or angiogenesis, determining the effectiveness of drugs, addetermining patient prognosis, or as targets for screening pharmaceutical agents that inhibit the growth or metastasis of tumour cells. The present sequence represents the human cancer associated phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETAGPSKTVSPVLSGSSRLSKDTETSVSEKELTQLAQIRPLIFNSSARSAMRDCLNTLQK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K-EELDIIREFLELEQMTLPDDFNSGNTLQNRDKNRYRDILPYDSTRVPLGKNKDYINAS 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YIRIVNHEEEYFYIATQGPLPETIEDFWQMVLENNCNVIAMITREIECGVIXCYSYWPIS 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKEPLEFEHFSVFLETFHVTQYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADF 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIKYVRYVRKSHITGPLLVHCSAGVGRIGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQR 398
                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POAQVFENKVNSEKVKLSLRNFPHNDYEDVFEEPSESGSDPSMWTARGPFRRDRWSSEDE 77
                                                                                                                                                                                                                                                                                                                                                                                                                    40 PIKPIFGNKANSENVKPSHHLSFSDKYELVYPRPLESDTDETVWDVSDRSLRNRWNSMDS
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          novel gene; novel protein; tissue marker; molecular weight marker;
chromosome marker; genetic disorder; contig.
                                                                                                                                                                                                                                                                                                                                                                        æ
                                                                                                                                                                                                                                                                                                                         Length 398;
                                                                                                                                                                                                                                                                                                                                                                        78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel protein-related contig polypeptide sequence #189
                                                                                                                                                                                                                                                                                                                    58.5%; Score 1310; DB 7;
65.4%; Pred. No. 9.9e-116;
ive 48; Mismatches 78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADE09123 standard; protein; 409
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11-DEC-2001; 2001US-0359453P.
14-MAR-2002; 2002US-036591P.
14-MAR-2002; 2002US-036584P.
12-APR-2002; 2002US-037281P.
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                                                                                                                                                                                                                                                                                                                                                                        253; Conservative
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                         Sequence 398 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCULT 9
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278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 LKKPLBLKHPRVFLENYQILQYFIIRWFQVVEKSTGTSHSVKQLQFTKWPDHGTPASADS 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       381
                                                                                                                                                                                                                                                                            The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present maino acid sequence was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88
                                                                                                                                                                              New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                 Wang J;
Wang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 PIXPIFGNKONSENVKPSHHLSFSDKYELVYPEPLESDTDETVWDVSDRSLRNRWNSMDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 POAQVFENKVNSEKVKLSLRNFPHNDYEDVFEEPSESGSDPSMWTARGPFRRDRWSSEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 BTAGPSKTVSPVLSGSSRLSKDTETSVSEKBLTQLAQIRPLIFNSSARSAMRDCLNTLQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 K-EBLDIIRBFLELEQMTLPDDFNSGNTLQNRDKNRYRDILPYDSTRVPLGKNKDYINAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 YIRIVNHEERYPYIATQGPLPETIEDFWQAVLENNCNVIAMITREIECGVIKCYSYWPIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKEPLEFEHFSVFLETFHVTQYFTVRVPQIVKKSTGKSQCVKHLQFTKWPDHGTPASADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIKYVRYVRKSHITGPLLVHCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIKYIRYARKSHLIGPMVVHCSAGIGRIGVFLCVDVVFCAIVKDCSFNIMDIVAQMREQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                               Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                 J, Zhao QA,
Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.5%; Score 1310; DB 7; Length 409; 65.4%; Pred. No. 1e-115; ive 49; Mismatches 78; Indels 8
                                                                               Zhang
                                                                                               Zhou P,
                                                                                                                                                                                                                                                Disclosure, SEQ ID NO 2667; 1177pp; English.
                                                                                               Weng G, Z
Boyle BJ;
                                                                                 Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGMVQTKEQYHFCYDIVLEVLRKLLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         399 CGMIQTKEQYQFCYBIVLEVLQNELAL
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                                                                             Tang YT, Asundi V, Goodrich Ri
Ghosh M, Xue AJ, Wehrman T, 1
Ma Y, Wang D, Chen R, Xu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG06042 standard; protein; 561
22-APR-2002; 2002US-00128558.
24-APR-2002; 2002US-0376045P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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les 253; Conservative
                                                                                                                                                WPI; 2003-569235/53.
                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 409 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches
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The invention relates to isolated polymucleotide (1) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity can not to produce other types of data and products dependent on DNA and anno acid sequences. ABG00010-ABG030377 represent novel human diagnostic partent did not appear in the printed specification, but was obtained in electronic format directly from MIPO at the printed specification, but was obtained in the wipe of the inventices.
                                                                                                                                                                                                                                                                                                                                                                     diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID NO 36401; 103pp; English.
                                                                                                                                     30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                         31-MAR-2000; 2000US-00540217, 23-AUG-2000; 2000US-00649167,
                                                                                                                                                                                                                                                                            Liu C,
                                                                                                                                                                                                                                                                                                                     WPI; 2001-639362/73
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Matches 252; Conserv
                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC
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                                                         WO200175067-A2.
                     Homo sapiens.
                                                                                                                                                                                                                                                                            Drmanac RT,
                                                                                               11-OCT-2001
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44 IFGN:WNSENVKPSHHLSFSDKYELVYPEPLESDTDETVWDVSDRSLRNRWNSMDSETAG 103 244 104 PSKTVSPVLSGSSRLSKDTETSVSEKELTQLAQIRPLIFNSSARSAMRDCLNTLQKK-EE 162 282 222 298 YDIMQEFWALELKNIPGEFYSGNQPSNREKNRYRDILPYDSTRVPLGKSKDYINASYIRI 357 417 477 LEFEHPSVFLETFHVTQYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKY 342 163 LDIIREFLELEQMTLPDDFNSGNTLQNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRI 223 VNHBEBYFYIATQGPLPETIEDFWQMVLENNCWVIAMITREIBCGVIKCYSYWPISLKEP VNCGEEYFYIATQGPLLSTIDDFWQMYLENNSNVIAMITREMEGGIIKCYHYWPISLKKP .; ф 58.3%; Score 1306; DB 4; Length 561; 65.8%; Pred. No. 4.1e-115; ive 48; Mismatches 75; Indels 8 252; Conservative

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343 VRYVRKSHITGPLLVHCSAGVGRTGVPICVDVVFSAIEKNYSPDIMNIVTQMRKQRCGMI 402 425 538 OTKEQYHFCYDIVLEVLRKLLTL 560 403 OTKEQYOPCYEIVLEVLONLLAL 원 ò

AAE37994 standard; protein; 261 AAE37994

RESULT 11

2

AAE37994;

(first entry) 06-NOV-2003

Human kinase and phosphatase (KPP-39) protein.

mutations

Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis; atheroscierosis; cirrhosis; haemoglobinuria; polycythaemia vers; cancer; psoriasis; thromobocytopaemia; developmental disorder; Reiter's syndrome; renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease; nutoimmune disorder; Parkinson's disease; epilepsy; glomerulonephritis; autoimmune disorder; Parkinson's disease; epilepsy; glomerulonephritis; acquired immune deficiency syndrome; immunosuppressive; Crohn's disease; allorgy; gout; Grave's disease; multiple sclerosis; diabetes mellitus; allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome; osteoporosis; rheumatcid arthritis; Sjogren's syndrome; ophthalmological; gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.

Homo sapiens.

WO2003050084-A2.

19-JUN-2003

06-DEC-2002; 2002WO-US039126

07-DEC-2001; 2001US-0340235P. 19-DEC-2001; 2001US-0343007P. 21-DEC-2001; 2001US-034346P. 04-FEB-2002; 2002US-0357458P. 15-FEB-2002; 2002US-0357675P.

(INCY-) INCYTE GENOMICS INC.

Kable AB, Chien D, Wilson AD, Swarnakar A, Gorvad AB; Hafalia AJA, Emerling BM, Rankumar J, Jin P, Griffin JA, Marquis JP; Baughn MR, Chawla MK, Lehr-Mason PM, Khare R, Lee S, Hawkins PR; Becha SD, Lee SY, Sprague WW, Zebarjadian Y;

WPI; 2003-532894/50. N-PSDB; AAD57366. New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis, cancer or hepatitis.

Claim 1; Page 242; 282pp; English.

The invention relates to an isolated polypeptide, which is a human kinase and phosphatase (RPP). KPP agonists and antagonists are useful for diagnosing, treating or preventing disorders associated with aberrant expression of KPP, particularly cell proliferative disorders (e.g. arteriosclerosis, atherococlerosis, hapatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis, parimary thromobocytopaenia or cancer) developmental disorders (eg. renal tubular acidosis, anaemia or mental retardation), neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/inflammatory disorders (e.g. AlDS; acquired immune deficiency syndrome,

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allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's dispease, disbetees mellitus, glomerulonephitis; docdgasture's syndrome, gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome, multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's pyrdrome, rheumatoid arthritis, Sjogren's syndrome, uveritis), or vixal, bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP is useful in assessing the effects of exogenous compounds on the useful in gene therapy and for creating transgenic animals to model human disease. The present sequence is human KPP protein

Sequence 261 AA;

225 BEBYFYIATQGPLPETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEF 285 61 GEEFYTATQGPLLSTIDDFWQWYLENNSNVIAMITREIEGGIIKCYHYWPISLXXPLEL 120 EHPSVFLETFHVTQYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRY 345 405 9 166 IREFLELEQMILPDDFNSGNTLQNRDKNRYRDILPYDSTRVPLGKOKDYINASYIRIVNH 1 MOSFWALELKVLPGEFNSGNQPSNREKNRYRDILPYDSTRVPLGKSKDYINASYIRIVNC VRKSHITGPLLVHCSAGVGRTGVFICVDVVPSALEKNYSFDIMNIVTQMRKQRCGMIQTK Gaps ö Length 261; 35; Indels Query Match
47.8%; Score 1071; DB 6;
Best Local Similarity 75.8%; Pred. No. 3.1e-93;
Matches 197; Conservative 28; Mismatches 35; 226 346

EQYQFCYEIVLEVLQNLLAL 425 FOXHFCYDIVLEVLRKLLTL 406 241

SULT 12 367637

AAG67637 standard; protein; 1267 AA

AAG67637;

(first entry) 26-NOV-2001

Amino acid sequence of a human protein.

Human; protein kinase; protein phosphatase; signal transduction

Homo sapiens

WO200109316-A1

08-FEB-2001

28-JUL-2000; 2000WO-JP005061

29-JUL-1999; 99JP-00248036. 18-OCT-1999; 99US-0159590P. 11-JAN-2000; 2000JP-00118776. 17-FEB-2000; 2000US-0183322P. 02-MAY-2000; 2000JP-00183767. 09-JUN-2000; 2000JP-00241899.

(HELI-) HELIX RES INST

Saito K, Yamamoto J; Otsuki T, Funahashi S; Isogai T, Nishikawa T, Hayashi K, S Sugiyama T, Wakamatsu A, Nagai K, Ishii S, Senoo C, F

Human; protein kinase; protein phosphatase; signal transduction; intracellular signalling pathway.

WO200109345-A1

08-FEB-2001

Amino acid sequence of a human polypeptide.

(first entry)

26-NOV-2001

WPI; 2001-570286/64

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1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1126
                                                                                             is expected that the protein Kinase/protein phosphares gene participates in signal transduction in cells. The protein kinase/protein phospharase polypeptides and polynucleotides are useful for developing diagnostics and treatment agents for human and animal diseases. The protein kinase/protein phosphatase polypeptides are useful as target molecules in designing novel drugs. The protein kinase/protein phosphatase polymucleotides are useful as a source of probes and primers, which may be used to isolate homologous sequences. The present sequence represents a human protein, which is used in the course of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176
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                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                   human protein kinase/protein phosphatases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1067 PLPTTVGDFWQMIWEQKSTVIAAMTQEVEGEKIKCQRYWPNILGKTTWVSNRLRLALVRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 PLPETIEDFWOMVLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLETF
                                                                                                                                                                                                                                                                                                                                                                    6 KVRGKTGRDNDEEEGNSGNLNLRNSLP---SSSQKMTPTKPIFGNKMNSENVKPSHHLSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 BTSVSEKELTQLAQIRPLIFNSSARSAMRDCLNTLQ-----KKEELDIIREFLELEQMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 LPDDFNSGNTLQNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1127 QQLKGFVVRAMTLEDIQTREVRHISHIANFTAMPDHD7PSQPDDLLTFISYMRHIHRSGPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 HVTQYFTVRVFQIVKKSIGKSQCVKHLQFTKWPDHGTPASADFFIKYVRVVRKSHITGPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVHCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIV
                                                                                                                                                                                                                                                                                                                                       Gaps
 New genes encoding proteins with protein kinase/protein phosphatase activity, useful in the diagnosis and treatment of diseases.
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                                                                                                                                                                                                                                                                                                                                                                                           Length 1267;
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                  29.2%; Score 653.5; DB 4; 34.7%; Pred. No. 2.3e-52; tive 73; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Page 206-215; 233pp; Japanese
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                                                                                                                                                                                                                                                                                                                  Local Similarity 34.73 tes 149; Conservative
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                                                                                                                                                                                                                                                                  Sequence 1267 AA;
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Page 10

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The specification describes human protein kinase/protein phosphatases. The polypeptides are expected to participate in signal transduction in cells. The kinase phosphatases are connected with intracellular signalling pathways. Antisense oligonuclectides and compounds identified by screening (agonists or antagonists) can be used to treat human or animal disorders associated with the expression or function of the protein. In addition, the polypeptides may be used as target molecules fir drug development. The present sequence represents a polypeptide, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : :: | | :: | | :| | :: | | : : | | : : | | : : | | | : : | | | : : | | | : : | | | : | | | : | | | : | | | : | | | : | | | : : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | : | | | : | | : | | | : | | : | | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   hikawa I, Hayashi K, Saito K, Yamamoto J;
Wakamatsu A, Nagai K, Otsuki I, Funahashi S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New genes encoding protein kinase and protein phosphatase, useful for identifying modulators which can be used to treat human or animal disorders associated with the expression or function of these enzymes.
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                                                                                                                                                                                                                                                                                                                                                                                       . Sugiyama T, Nakamatr.
Nezu J;
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                                                                                                                                                           18-OCT-1999; 99US-0159590P.
11-JAN-2000; 2000JP-00118776.
17-FEB-2000; 2000US-0183322P.
                                           28-JUL-2000; 2000WO-JP005060
                                                                                                                                                                                                                                                                                   02-MAY-2000; 2000JP-00183767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1267 AA;
                                                                                                                    29-JUL-1999;
18-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ishii S,
Senoo C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     872
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The invention relates to a complex between two interacting proteins in adipocyte cells, given in the specification. The proteins are identified by selecting a bait protein from a known adipocyte marker and then performing a bait protein from a known adipocyte marker and then performing a peast 2-hybrid selection to isolate prey proteins encoded by members of an adipocyte cDNA library. The proteins are designated SID (RTM) (selected interacting domains) proteins. Also included are a polymucleotide encoding a polypeptide in the adipocyte cells, a combinant host cell expressing at least one of the interacting polypeptides of the complex, selecting a modulating compound in adipocyte cells, a SID (RTM) polymetride comprising any of the 738 amino acid sequences given in the specification (including its fragment or variant), a vector comprising the Specification (including its fragment or variant), a vector comprising the vector, a protein chip comprising the polymetrides and compounds are useful for recomplex, polypeptides, polymetcleotides and compounds are useful for preventing or treating metabolic disorders such as obesity or diabetes. The complex, polymetolectides and compounds are useful for The polymetolectides and compounds are useful for The polymetolectide interacting domains (SID (RTM) tring the therapeutic effect. The present sequence represents a SID (RTM) between the protein interaction, thus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   370 KANGKLSBERTEDTDCDG----SPLPEYFTEATKANGCEEYCEEKVKSESL----- 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New complex between two interacting proteins in adipocyte cells, useful for identifying selected interacting domains that modulate protein interactions, or for preventing or treating metabolic disorders such as obesity or diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 KVRGKTGRDNDBEBGUSGNLALRNSLP---SSSQKMTPTKP1FGNXMNSENVKPSHHLSF
                                                                                                                                                                                     Human, prey, adipocyte, SID, selected interacting domain, anorectic, antidiabetic, protein-protein interaction; diabetes, yeast 2-hybrid assay; metabolic disorder; obesity.
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34.7%; Pred. No. 1.2e-52;
iive 73; Mismatches 152; Indels
                                                                                                                                                Human adipocyte Selected Interacting domain, SID, #319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 208-209; 382pp; English.
                        ABU70688 standard; protein; 766 AA
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                                                                 ABU70688;
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                                                                                                                      GPLPETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLET 294
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                                                                                                                                                                       295 FHVTQYFTVRVPQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGP
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----IQKPQEKKTDDDEITWG-NDELPIERTNHEDSD---
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745 ILYVLTRLQA 754
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05-OCT-1995
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A cDNA library was prepd. from human glioma cell line U-343 MGa 31L or AG1518 human foreskin fibroblasts. Degenerate primers based on conserved regions of PTPs were prepd. Sense oligos were AAO85926 and AAO85927, and the antisense oligo was AAO85928. Three clones defined novel PTP sequences. Two of these were named PTPL1 and GLM-2. The U-343 MGa 31L

New protein tyrosine phosphatase(s), PTPL1 and GLM-2 - used to develop prods. for use in detection, diagnosis, screening assays or therapy.

WPI; 1995-115450/15 N-PSDB; AAQ85924 Claim 9; Page 56-68; 92pp; English.

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2117 ----IQKPQEXKTDDDEITWG-NDELPIERTNHEDSD-------KD- 2150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 ETSVSEKELTQLAQIRPLIFNSSARSAMRDCLNTLQ-----KKEELDIIREFLELEQM 175
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CDNA library was screened with labeled probes corresp. to PTLP1. The AGISTB human fibroblast cDNA library was also screened. The complete C of PTPL1 was derived from alx overlapping CDNA clones and is given in AAQSS924. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                         6 KVRGKTGRDNDEBEGNSGNINILRNSI.P---SSSOKMTPTKPIFGNKMNSENVKPSHHLSF
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Copyright (c) 1993 - 2004 Compugen Ltd.
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PCT-US94-0943-2

US-09-290-640-46

US-09-848-294-7

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US-08-848-294-7

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US-08-848-294-7

US-08-848-294-7

US-08-868-5

US-09-444-3

US-09-444-533-2

PCT-US9E-05512-2

US-08-416-64-3

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US-08-087-244A-8
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ਜੇਜੇਜੇਜੇਜੇਜੇਜੇਨ ਨਿਹਿਨ ਜਿ		PPLICATION US 21075 GONEZ, LEON GONEZ, JAN CLARESSON-WE HELDIN, CAR NVENTION: EX NVENTION: EX NVENTION: TY SEQUENCES: E GOO ATLANTIO COSTON ATLANTION DATA: COSTON ATLANTION ATLANTICATION ATLAN
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Score 653; DB 2; Length 2465; Pred. No. 1.2e-53;

29.18; 34.78;

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Patent No. 6066472

GENERAL, INFORMATION:
APPLICANT: GENES, JAN
APPLICANT: CLASSON-WELSH, LENA
APPLICANT: HELDIN, CARL-HENRIN
TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                   63 SDKYELVYPEPLESDIDETVMDVSDRSLRNRMNSMDSETAGPSKTVSPVLSGSSRLSKDT 122
                                                                                                                                                                                                                              123 ETSVSEKELTQLAQIRPLIFNSSARSAMRDCLNTLQ-----KKBELDIIREFLELEQM 175
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                                              6 KVRGKTGRDNDEEEGNSGNLNLRNSLP---SSSQKMTPTKPIFGNKMNSENVKPSHHLSF
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  26;
  73; Mismatches 152; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,804
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CLASSIPICATION:
PRIOR APPLICATION NATA:
APPLICATION NUMBER: US 08/596,291
FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION UNDER: PCT/US94/09943
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
CMEDTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Matches 149; Conservative
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CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
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APPLICANT: Saras, Jan
APPLICANT: Saras, Jan
APPLICANT: Franzn, Petra
APPLICANT: Aspenstrm, Pontus
APPLICANT: Gonez, Leonel Jorge
APPLICANT: Gonez, Leonel Jorge
APPLICANT: Gonez, Leonel Jorge
APPLICANT: Heldin, Carl-Henrik
ITLLE REFERRACE: L0461/7030
CURRENT APPLICATION NUMBER 105/09/080,855A
CURRENT FILING DATE: 1998-05-18
SARLIER APPLICATION NUMBER: 08/805,583
SARLIER APPLICATION NUMBER: 08/805,583
SARLIER PILING DATE: 1997-02-25
NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 ETSVSEKELTQLAQIRPLIFNSSARSAMRDCLNTLQ-----KKEELDIIREFLELEOM 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 TLPDDFNSGNTLQNRDKNRYRDILPPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQ 235
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                                                                                                                                                                                                                                                                                                                  29.1%; Score 653; DB 3; Length 2465; 34.7%; Pred. No. 1.2e-53; tive 73; Mismatches 152; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: L0461/7003
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEFX: 17-720-2441
TELEFX: SEQUENCE CHARACTERISTICS:
LENGTH: 2465 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-080-855-12
; Sequence 12, Application US/09080855A
; Patent No. 6083721
                                                                                                                                                                                                                                                                                                                      Query Match 29.1
Best Local Similarity 34.7
Matches 149; Conservative
GATES, EDWARD R.
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2444 ILYVLTRLQA 2453
                                                                                                                                                                                                           ; TYPE: amino acid
; TOPOLOGY: linear
; MOLEGULE TYPE: protein
US-09-100-804-3
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                                                                                                                                                                                                                                                                                                                                                                                                             236 GPLPETIEDFWOMVLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLBFBHFSVFLET 294
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                                                                                                                                    123 ETSVSEKELTQLAQIRPLIFNSSARSAMRDCLNTLQ-----KKEBLDIIREFLBLBQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 PHVTQYFTVRVPQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGP
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COUNTRY: USA
COUNTRY: USA
COMPUTER: READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US94/09943
FILING DATE: 01-SEP-1994
                                    FILING DATE: 01-SEP-1994
CLASSIFICATION
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
ATTORNEY/GREWIT INFORMATION:
NAME: TWOMEY, MICHAEL J.
REGISTRATION NUMBER: P-38,349
REGISTRATION NUMBER: P-38,349
TELECOMMULCATION INFORMATION:
TELEPENNE: 617/720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application PC/TUS9409943 GENERAL INFORMATION:
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STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
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TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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APPLICANT: Sazas, Jan
APPLICANT: Parazn, Petra
APPLICANT: Appension, Detra
APPLICANT: Hellman, Ulf
APPLICANT: Gonez, Leonel Jorge
APPLICANT: Heldin, Carl-Henrik
TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPLI
TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPLI
TITLE OF INVENTION: DAG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPLI
TITLE OF INVENTION OWNER: US/09/566,076
CURRENT FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2150
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                                                                                                          Length 2466;
                                                                                                       Query Match

29.1%; Score 653; DB 3; Length 246
Best Local Similarity 34.7%; Pred. No. 1.2e-53;
Matches 149; Conservative 73; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2117 ----IQKPQEKKTDDDEITWG-NDELPIERTNHEDSD----
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       ORGANISM: Homo sapiens
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2170 HSFLTNDELAVLPVVKVLPSGKYTGANLKSVIRVLRGLLDQGIPSKELENLQELKPLDQC 2229
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Patent No. 6653133
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US-09-665-615B-46
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Sequence 46. Application US/09290640
Patent No. 6204055
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling FILE REPERSENCE: 128H-0351
CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 46
                                                                                           6
                                                                                                                                                                                                                                                                                                                                      176 TLPDDFNSGNTLQNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEFFYIATQ 235
2211 LI-----GQTKENRRKNRYRNILPYDATRVPLGDEGGYINASFIKIPVGKEBFVYIACQ 2264
                                                                                                                                                                                                                                                                                                                                                                                                                                  355 LLVHCSAGVGRIGVFICVDVVPSAIEXNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEI 414
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                                                                                                                                                                                                  63 SDKYBLVYPEPLESDIDETVWDVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSKDT 122
                                                                                                                                                                                                                                                                                                                                                                                                           GPLPETIEDFWOMVLENNCNVIAMITREIECGVIKCYSYMPISL-KEPLEFEHFSVFLET 294
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                                                                                                                                                              2070 KANGKLSEERTEDTDCDG----SPLPEYFTEATKANGCBEYCBEKVKSESL-----
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                                                                                                                             6 KVRGKTGRDNDEBEGNSGNLNLRNSLP---SSSOKWTPTKPIFGNKMNSENVKPSHHLSF
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29.1%; Score 653; DB 3; Length 2485;
Best Local Similarity 34.7%; Pred. No. 1.2e-53;
Matches 149; Conservative 73; Mismatches 152; Indels 5
                                                           Length 2466;
                                                         Query Match 29.1%; Score 653; DB 5; Length 246 Best Local Similarity 34.7%; Pred. No. 1.2e-53; Matches 149; Conservative 73; Mismatches 152; Indels
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       MOLECULE TYPE: protein
CT-US94-09943-2
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                      GPLPETIEDFWOMVLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLET 294
176 TLPDDFNSGNTLQNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQ 235
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                                                                             355 LLVHCSAGVGRTGVPICVDVVPSALBKNYSPDIMNIVTOMRKORCGMIQTKRQYQPCYBI
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APPLICANT: Marcusson, Exic G.
APPLICANT: Marcusson, Exic G.
APPLICANT: Wyatt, Jacqueline
TITLE OF INVENTION: Antisense Modulation of Fas Mediated Signaling
TITLE OF INVENTION: Antisense Modulation of Fas Mediated Signaling
TITLE OF INVENTION: ANTISENSE WOOD 18
CURRENT APPLICATION NUMBER: US/09/665,615B
CURRENT FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: US 09/290,640
PRIOR APPLICATION NUMBER: US 09/290,640
NUMBER OF SEQ ID NOS: 179
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 46
LENGTH: 2485
TYPE: PRT
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29.1%; Score 653; DB 4; Length 2485;
Best Local Similarity 34.7%; Pred. No. 1.2e-53;
Matches 149; Conservative 73; Mismatches 152; Indels 5
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890 QYKFVCEAILRVYE 903
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US-08-348-006B-5
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Best Local S:
Matches 101
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TITLE OF INVENTION: Isolation of A cDNA Encoding A No. 6479640el

TITLE OF INVENTION: Isolation of A cDNA Encoding A No. 6479640el

TITLE OF INVENTION: Protein Tyrosine Phosphotase Which Localizes to Focal

TITLE OF INVENTION: Adhesions and Uses Therefor

FILE REFERENCE: CSHL90-04FZA

CURRENT APPLICATION NUMBER: US/09/848,294

CURRENT FILING DATE: 1999-01-22

PRIOR FILING DATE: 1999-01-22

PRIOR PPLICATION NUMBER: 08/159,536

PRIOR PLING DATE: 1999-02-04

PRIOR PLING DATE: 1999-03-08-16

PRIOR APPLICATION NUMBER: 07/663,579

PRIOR APPLICATION NUMBER: 07/663,579

PRIOR PILING DATE: 1991-03-01

PRIOR PILING DATE: 1991-03-01

PRIOR PILING DATE: 1991-03-01

SROFTWARE: PARLICATION NUMBER: 07/494,036

PRIOR FILING DATE: 1990-03-14

NUMBER: OF SEQ ID NOS: 13

SOFTWARE: PARLICATION NUMBER: 07/494,036

PRIOR FILING DATE: 1990-03-14

NUMBER: OF SEQ ID NOS: 13

SOFTWARE: PARLICATION NUMBER: 07/500-03-14

NUMBER: OF SEQ ID NOS: 13

SEQ ID NO 2: 12

FENTING DATE: 1990-03-14
                             2404 IITHCSAGIGRSGTLICIDVVLGLISQDLDFDISDLVRCKRLQRHGMVQTEDQYIFCYQV 2463
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     LLVHCSAGVGRTGVFICVDVVPSAIBKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYBI 414
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                                                                                                                                                                                                                                                     3-09-848-294-2
Sequence 2, Application US/09848294
Patent No. 6479640
GENERAL INFORMATION:
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2464 ILYVLTRLQA 2473
                                                                                                      415 VLEVLQNLLA 424
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ORGANISM: Homosapiens
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Best Local Similarity
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242 IEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEH--FSVFLETFHVTQ 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 NRDKNRYRDILPYDSTRVPLGKNKDYINASYI-----RIVNHEBEYFYIATQGPLPET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38;
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Patent No. 5658756
GENERAL INFORMATION:
APPLICANT: RODAN, GIDEON A.
APPLICANT: RUILD AZXIEL
APPLICANT: RUILEDGE, SU JANS
ITILE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
ITILE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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STREET: 126 B. LINCOLN AVE., P.O. BOX 2000
CITY: RAHWAY
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07065-0900

us-09-095-478a-5.rai

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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 LELEQMILPDD-----FNSGNTLQNRDKARYRDILPYDSTRVPLG-----KNKDYINAS 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 YIRIVNHEEEYFYIATQGPLPETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPIS 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 LKEPLEFEHESVF-LETFHVTQYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASAD 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
21.9%; Score 490.5; DB 1; Length 1911;
Best Local Similarity 40.2%; Pred. No. 4.9e-38;
Matches 107; Conservative 47; Mismatches 91; Indels 21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08800825A
Patent No. 586537
GENERAL INFORMATION
APPLICANT: SCHMIDY, AZRIEL
APPLICANT: SCHMIDY, AZRIEL
APPLICANT: RUTLEDGE, SU JANA
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,006B
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126 E. LINCOLN AVE., P.O. BOX 2000
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                                                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
8 FILING DATE: 14-SEP-193
ATTORNEY/AGENT INFORMATION:
NAME: HAND: 1, MARK
RESISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 189921A
TELEPHONE: 908-594-3905
TELEPHONE: 908-594-720
                                  ZIP: 07005-000 PRM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 1911 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
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CITY: RAHWAY
STATE: NEW JER
                                                                                                                                                                                                            FILING DATE
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JS-08-800-825A-5
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1818 GFIDFIGQVHKTKEQFGQDGPISVHCSAGVGRTGVFITLSIVLBRMRYEGVVDIFQTVKM 1877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.9%; Score 490.5; DB 2; Length 1911;
40.2%; Pred. No. 4.9e-38;
tive 47; Mismatches 91; Indel9 21; Gaps
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Patent No. 2214564
GENERAL INFORMATION:
APPLICANT: SCHNIDT, AZELEL
APPLICANT: SCHNIDT, AZELEL
APPLICANT: GINVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
ITILE OF INVENTION: TYROSINB PHOSPHATASE
NUMBER OF SUCHENCES:
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPLIAGATION NUMBER: US/08/800,825A
FILING DATE: 14-FEB-1997
CLASSIPICATION: 435
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126 E. LINCOLN AVE., P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              394 MRKQRCGMIQTKEQYQFCYEIVLEVL 419
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WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J. MARK.
REGISTRATION NUMBER: 36,545
REFRERNCE/DOCKET NUMBER: 1899;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3905
TELEFAX: 732-594-3726
                                                                                                                                                                                                                                                                                                                                                    TRLEFAX: 732-594-4720
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1911 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 40,2%
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
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07065-0900
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CITY: RAHWAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: NE COUNTRY:
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Best Local S
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.9%; Score 490.5; DB 3; Length 1911; 40.2%; Pred. No. 4.9e-38; tive 47; Mismatches 91; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: RODAN, GIDEON A
APPLICANT: RODAN, GIDEON A
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JAME
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES:
ADDRESSE: JOHN W. WALLEN III
STREET: ADDRESSE: JOHN W. WALLEN III
STREET: RAHWAY
STREET: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patemetur Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10166
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158,657
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                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/800,825
FILING DATE: 14-FEB-1997
ATTORNEY-AGENT INFORMATION:
NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REGISTRATION NUMBER: 36,545
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application PC/TUS9410166
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 1911 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 40.2% Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein 3-09-158-657-5
                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                          CLASSIFICATION:
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170 LELEQMTLPDD-----FNSGNTLQNRDKNRYRDILPYDSTRVPLG-----KNKDYINAS 218
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21.9%; Score 490.5; DB 5; Length 1911;
Best Local Similarity 40.2%; Pred. No. 4.9e-38;
Matches 107; Conservative 47; Mismatches 91; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 37, Application US/08446345
| GENERAL INFORMATION:
| APPLICANT: Willish P.H.
| APPLICANT: Moller, Karin B. TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE TITLE OF INVENTION: PHOSPHATASES PTP-D1
| NUMBER OF SEQUENCES: 41
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Pennie & Edmonds | ADDRESSEE: Pennie & Edmonds | ADDRESSEE: Pennie & Edmonds | ADDRESSEE: Pennie & Edmonds | ADDRESSEE: Pennie of the Americas | CITY: New York | STARTS: N.Y.
| COUNTRY: U.S.A. | CONNTRY: U.S.A. | CONNTRY: U.S.A. | CONNTRY: U.S.A. | CONNTRY: READABLE FORM: MEDIUM TYPE: Floppy disk | COMPUTER: IBM PC COMPATIBLE | COMPATIBLE | PATCHIN RELEASE | #1.0, Version #1.25 | CURRENT APPLICATION NATA.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,032
FILING DATE: 14-SEP-1993
ATTORNEY AGENT INFORMATION:
NAME: WALLEN, JOHN W III
REGISTRATION NUMBER: 35403
REPERENCE/DOCKET NUMBER: 18992
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
TELEFAX: 908-594-305
TELEX: 138225
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APPLICATION NUMBER: US/08/446,345
PILING DATE: 22-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1911 amino acids
TYPE: amino acid
STRANDBDNBSS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 IEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEH-FSVFLETFHVTQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSAGVGRIGVPICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYBIVL 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 231;
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GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas

APPLICANT: Flint, Andrew J.

TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN

TITLE OF INVENTION: TYROSINE PHOSPHATASES

NUMBER OF SEQUENCES: 36

CORRESCOUDENCE ADDRESS:

ADDRESSES: HAMILTON, BROOK, SMITH & RETNOLDS, P.C.

STREET: Lexington

STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.8%; Score 489; DB 2;
42.0%; Pred. No. 2.3e-39;
tive 37; Mismatches 83.
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OPERATING SYSTEM: Windows 95
SOFTWARE: FESTENG for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/234,440
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LBULR A 30/42
REGISTRATION NUMBER: 30/42
REPERSNEK/DEOCKET NUMBER: 30/42
TELEPHONE: (212) 790-909
TELEPAX: (212) 869-8864
TELEX: 66.141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
FUNCHAL SEG ID NO: 37:
FUNCHAL SEG ID NO: 37
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25-JUL-1996
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| Sequence 21, Application US/08685992
|Patent No. 5912138
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ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 21.8 Best Local Similarity 42.0 Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: protein
S-08-446-345-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: unb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH
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188 ONRDKONRYRDILPYDSTRVPLGKUKDYINASYI-----RIVNHEBESYFYIATQGPLPR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 TIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHV--- 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 TCAQFWQVVWDQKLSLIVMLTTLTERGRTKCHQYWP---DPPDVWNHCG-----FHIQCQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 SEDCTIAVVSMLVTNTQTGEEHTVTHLQYVAWPDHGIPDDSSDFLEFVNYVRSLRVDSEP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355 LLVHCSAGVGRTGVFICVDVVPSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEI 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 TOYFTVRVPQ--IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHI-TGP
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          56;
                                                                                                                                                                                                                                                                                                                                                                     Query Match 21.7%; Score 487; DB 2; Length 242; Best Local Similarity 41.8%; Pred. No. 3.8e-39; Matches 102; Conservative 37; Mismatches 79; Indels
REFERENCE DOCKET NUMBER: 32,227
REFERENCE DOCKET NUMBER: CSHL96-03
TELECOMMUNICATION INPORMATION:
TELEPAK: 781-861-6240
TELEPAK: 781-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: June 16, 2004, 13:25:27 Job time: 25 secs
                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 VLEV 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 ILRV 241
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RESULT 1
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Sequence 3, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 35, Appli
Sequence 12, Appl
Sequence 12, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 12, Appli
Sequence 14, Appli
                                                                                                                                                                                       June 16, 2004, 13:24:26 ; Search time 48 Seconds (without alignments) 2500.319 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                      2241
1 MSSPRKVRGKTGRDNDEEBG.....QYQFCYEIVLEVLQNLLALY 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/ReT_Ray PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/ReT_Ray PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9F_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9F_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO9F_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO9F_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO9F_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USIOB_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USIOB_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USIOB_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/USIOB_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USIOB_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USIOB_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USIOB_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USIOB_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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0 US-09-095-478-2

0 US-09-095-478-8

0 US-09-095-478-6

0 US-09-095-478-6

0 US-09-095-478-6

0 US-09-095-478-4

1 US-10-01-478-4

1 US-10-060-065-35

4 US-10-059-585-56

4 US-10-177-980-12

US-10-177-980-12

US-10-177-980-12

US-10-177-980-12

US-10-177-980-12

US-10-177-980-12

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US-10-177-980-12

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US-10-177-980-13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1158786 segs, 281726120 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            >st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                            4 protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .nimum DB seq length: 0 iximum DB seq length: 20000000000
                                                                                                                                                                                                                                                                                                                       US-09-095-478A-5
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4426
4212
4212
4220
4248
4485
4485
3488
358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       coring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sarched:
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ALIGNMENTS

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RESULT 1

SGGUEGOE 1, Application US/08095478

Publication No. US2003009597041

GENERAL INPORMATION:
APPLICANT: Plowman, Gregory
TITLE OF INVENTION:
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION:
STREET: SUITE 4700
CITY: LOS Angeles
STREET: Suite 4700
CUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" DISKETTE, 1.49
MEDIUM TYPE: 3.5" DISKETE, 1.44 Mb
MEDIUM TYPE:
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264
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                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SFSDKYELVYPEPLESDTDETVWDVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FNSGNTLQNRDKWRYRDILPYDSTRVPLGKWKDYINASYIRIVWH3EEYFYIATQGPLPE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 FWSGYTLQNRDKORYRDILPYDSTRVPLGKNKDYINASYIRIVWH3EEEYFYIATQGPLPE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 IISDEWQWVLENKUVVZAMITREIBCGVIKCYSYWPISLKEPIEREHFSVPLETFHVTQY 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 TIEDEWGMYJENNCNVIAMITREIECGVIKCYSYMPISLKEPIERFSVFLETFHVTQY 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTVRVFQIVKKSTGKSQCVKHLQPTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 FTVRVPQIVKKSTGKSQCVKHLQPTKMPDHGTPASADFPIKYVRYVRKSHITGPLLVHCS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 AGVGRTGVPICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 AGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ 420
                                                                                                                                                                                                                                                                                                                                                   1 MSSPRKVRGKTGRDNDEEEGNSGNINLRNSLPSSSQKOATPTKPIFGNIKMNSENVKPSHHL 60
                                                                                                                                                                                                                                                                                                                            1 MSSPRKVRGKTGRDNDEEEGNSGNLNLRNSLPSSSQXMTPTKPIFGNXMNSENVKPSHHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DTETSVSEKZELTQLAQIRPLIFNSSARSAMRDCLNTLQKKEBLDIIREFLELEQMTLPDD
                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                     100.0%; Score 2241; DB 10; Length 426; 100.0%; Pred. No. 2.5e-194; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09095478
Publication No. US20030095970A1
GENERAL INPORMATION:
APPLICANT: PLOWMEN:
TITLE OF INVENTION: PHOSPHATASE SUPTPOS AND
TITLE OF INVENTION: PHOSPHATASE SUPTPOS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSPEN Mest Fifth Street
STREET: 633 West Fifth Street
STREET: Galife 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5° Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 426; Conservative
                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 NLLALY 426
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IS-09-095-478-2
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181 SSARSAMRDCLNTLOKKEBELDIIRBFLELECOMTLEDDFNSGNTLONRDKNRYRDILPYDS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VFLLIKTIMYNVFKLWKGKLIFGNKYNSENVKPSHHLSFSDKYELVYPEPLESDTDETVW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 IECGVIKCYSYWPISLKEPLEFERFSVFLETFHVTQYFTVRVEQIVKKSTGKSQCVKHLQ 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 PTKWPDHGTPASADFPIKYVRYVRYVRKSHITGPLLVHCSAGVGRIGVFICVDVVPSAIBKNY 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 DVSDRSLRNRWNSMDSBTAGPSKTVSPVLSGSSRLSKDTETSVSEKELTQLAQIRPLIFN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQIVKKSTGKSQCVKHLQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 FIKWPDHGTPASADFFIKYYRYVRKSHITGPLLVHCSAGVGRTGVFICVDVVFSAIEKNY 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 TRVPLGKNKDYINASYIRIVNHEBEYFYIATQGPLFETIEDFWQMVLENNCNVIAMITRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 -------IPGNKMNSENVKPSHHLSFSDKYELVYPEPLESDTDETVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 SSARSAMRDCINTLOKKEBLDIIREFLBLEQMTLPDDFNSGNTLQNRDKORYRDILPYDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 98.7%; Score 2212.5; DB 10; Length 463; Best Local Similarity 92.0%; Pred. No. 1.1e-191; Matches 426; Conservative 0; Mismatches 0; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 SFDIMNIVTOMRKORGMIQTKEOYOFCYBIVLEVLONLALY 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384 SPDIMNIVFOMRKORCGMIQTKEOYOFCYEIVLEVLONLLALY
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NOVEL PROTEIN TYROSINE
PHOSPHATASE SUPTPOS AND
RELATED PRODUCTS AND
METHODS
                            US/09/095,478
CURRENT APPLICATION
PAPPLICATION NUMBER: US/09/095,47
FILING DATE:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
ATORNEY/AGENT INFORMATION:
NAME: WAIDLING, BACANTON NUMBER: 32,327
REGISTRATION NUMBER: 224/1
REGISTRATION NUMBER: 224/1
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERIFICS:
LENGTH: 463 amino acide
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Publication No. US20030095970A1
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOYI TITLE OF INVENTION: PHOC TITLE OF INVENTION: RELY TITLE OF INVENTION: METHORSER OF SEQUENCES: 25 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
TOPOLOGY: linear
WOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
US-09-095-478-3
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GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE SUPPOS AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: RETHODS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: Suite 4700

CITY: Los Angeles STATE: California COUNTRY: U.S.A.

Publication No. US20030095970A1

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180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 FNSGNTLQNRDKORYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 TIEDEWQMVLENNCNVIAMITREIBCGVIKCYSYWPISLKEPLEPEHFSVFLETFHVTQY 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 FIVRVEQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSSPRVVRGKTGRDNDEEEGNSGNLNLRNSLPSSSQKMTPTKPIFGNKMNSENVKPSHHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DTETSVSEKELTQLAQIRPLIFNSSARSAMRDCLNTLQKKEELDIIREFLELEQMTLPDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 FNSGNTLQNRDKARYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEFYYLATQGPLPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.2%; Score 2133; DB 10; Length 412; 100.0%; Pred. No. 1.5e-184; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 AGVGRIGVFICVDVVPSAIBKNYSFDIMNIVTQMRKQRCGMIQTK 405
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                                                                                                                          PILING DATE:
CLASSIFUCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: Warburg, Richard J.
REGISTAATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/;
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION OF SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
TYPE: amino acid
TYPE: amino acid
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 95.2
Best Local Similarity 100.
Matches 405; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
S-09-095-478-3
                                                              CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 EEBYPYIATOGPLPETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 GNKMINSENVKPSHHLSPSDKYELVYPEPLESDTDETVWDVSDRSLRNRWNSMDSETAGPS 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IRBFLELEQMTLPDDPNSGNTLQNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNH 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 IREFLELEGMTLPDDFNSGNTLQNRDKARYRDILPYDSTRVPLGKNKDYINASYIRIVMH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 EHFSVFLETPHVTQYPTVRVPQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRY 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VRKSHITGPLLVHCSAGVGRIGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GNGMYSENVKPSHHLSFSDKYELVYPEPLESDTDETVMDVSDRSLRNRWNSMDSETAGPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RHPSVFLETFHVTQYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRY
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ZIP: 90071-2066
ZIP: 90071-2066
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 5.5" Diskette, 1.44 Mb MEDIUM TYPE: 5.5" Diskette, 1.44 Mb MEDIUM TYPE: 5.5" Diskette, 1.64 Mb MEDIUM TYPE: 5.5" Diskette, 1.64 Mb COMPARTS: FastSEQ for Windows 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/095,478
                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WATCHDIG J.
REPERENCE/DOCKET NUMBER: 22,327
REPERENCE/DOCKET NUMBER: 22,327
REPERENCE/DOCKET NUMBER: 22,4115
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELERAX: 67-3510
INPORMATION POR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: Peptide
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ESULT 4 S-09-095-478-8 Sequence 8, Application US/09095478

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61 SPSDKYELVYPEPLESDTDETVWDVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSK 120
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                                                                                        181 ENNCNVIAMITREIECGVIKCYSYWPISLKEPLEPEHFSVFLETFHVTQYFTVRVPQIVK 240
                                                        KSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGVFI 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSSPRKVRGKTGRDNDEBEGNSGNLALRNSLPSSSGKATTPTKP1FGNKANSENVKPSHHL
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                                                                                                                                                                  371 CVDVVFSAIBKNYSPDIMNIVTOMRKORCGMIQTKEOYOFCYBIVLEVLONLLA 424
301 CVDVVFSAIBKNYSFDIMNIVTOMRKORCGMIQTKEOYOFCYBIVLEVLONLLA 354
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Best Local Similarity 64.1%; Pred. No. 1.2e-118;
Matches 273; Conservative 53; Mismatches 92; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: INCTES GENOMICS, INC.; AU-YOUNG, Janice K. APPLICANT: BAUGHN, Mariah R.; DING, Li
APPLICANT: BAUGHN, Mariah R.; DING, Li
APPLICANT: GELFETN, Vicki S.; GANDHI, Ameena R.
APPLICANT: GELFETN, Jennifer A.; HAFALIA, April J.A.
APPLICANT: KEARNEY, Liam; LEB, Errestine A.
APPLICANT: AGVICU, Chandra S.; RAMKUMAR, Jayalaxmi
APPLICANT: REDDY, Roopa M.; SANJANALA, Madhusudan M.
APPLICANT: REDDY, Roopa M.; SANJANALA, Madhusudan M.
APPLICANT: TENARLY BIzabeth A.; TANG, Y. Tom
APPLICANT: TENARLY Michael B.; TRIBOULEY, Catherine M.
APPLICANT: TRANDA, Marinder K.; YANG, Junming
APPLICANT: TAOMIQUE G.; VUE, Henry
ITILE OF INVENTION: PROTEIN PROSENTANESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature; OTHER INFORMATION: Incyte ID No. US20040023245A1 7476861CD1 US-10-311-764-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: PI-OLZG USG

CURRENT APPLICATION NUMBER: US/10/311,764

CURRENT FILING DATE: 2002-12-16

PRIOR APPLICATION NUMBER: US 0/1/0301/1942

PRIOR FILING DATE: 2001-06-14

PRIOR PILING DATE: 2000-06-16

PRIOR PILING DATE: 2000-06-22

PRIOR PILING DATE: 2000-06-22

PRIOR PILING DATE: 2000-06-22

PRIOR PILING DATE: 2000-06-29

PRIOR PILING DATE: 2000-06-29

PRIOR PILING DATE: 2000-06-29

PRIOR PILING DATE: 2000-07-06

PRIOR PILING DATE: 2000-07-06

PRIOR PILING DATE: 2000-07-12

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Publication No. US20040023245A1
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ORGANISM: Homo sapiens
                                                                 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 PEPLESDTDETVWDVSDRSLRNRWNSWDSFTAGPSKTVSPVLSGSSRLSKDTETSVSEKE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 LTQLAQIRPLIFNSSARSAMRDCLNTLQKKBELDIIREFLELEQMTLPDDFNSGNTLQNR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LTÇLAQIRPLIFUSSARSAMRDCLNTLQKKEBLDIIREFLELEQMTLPDDFNSGNTLQNR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 DKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQMVL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 PEPLESDIDETVWDVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSKDTETSVSRKE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.1%; Score 1862; DB 10; Length 354; 100.0%; Pred. No. 4.4e-160; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE SUPPOS AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: RETHODS
NUMBER OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STREET: Galifornia
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5° Diskette, 1.44 Mb
MEDIUM TYPE: 3.5° Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SPUTARE: FASISEG for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/3
TELECOMMUNICATION INFORMATION:
TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acids
TYPE: amino acids
                                                                         361 BOYOFCYBIVLEVLONLLA 379
                                                                                                                                                                                                                                   Sequence 6, Application US/09095478 Publication No. US20030095970A1
                                         406 EQYOFCYBIVLEVLONLLA 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 354; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IS-09-095-478-6
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APPLICANT: Ai Wakamateu
APPLICANT: Keiichi Nagai
APPLICANT: Keiichi Nagai
APPLICANT: Shin-Ichi Funahashi
APPLICANT: Shin-Ichi Funahashi
APPLICANT: Chiaki Senoo
APPLICANT: Unn-Ichi Nezu
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE
FILE REPERRANCE: 06501-099002
CURRENT APPLICATION NUMBER: US/10/060,065
                     244 DFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTV 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 SDKYELVYPEPLESDTDETVWDVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSKDT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 ETSVSEKELTQLAQIRPLIFNSSARSAMRDCLNTLQ-----KKEELDIIREFLELEQMT 176
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                                           1 DFWQWVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           872 KANGKLSEERTEDTDCDG----SPLPEYFTEATKANGCEEYCEEKVKSESL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 KVRGKTGRDNDEREGNSGNLNLRNSLP---SSSQKMTPTKPIFGNKMNSENVKPSHHLSF
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PRIOR PILLING DATE: 2000-07-28.

PRIOR PILLING DATE: 2000-07-28.

PRIOR PILLING DATE: 1999-10-18.

PRIOR APPLICATION NUMBER: US 60/183,322.

PRIOR APPLICATION NUMBER: US 60/183,322.

PRIOR APPLICATION NUMBER: US 60/183,322.

PRIOR PILLING DATE: 2000-02-17.

PRIOR PILLING DATE: 1999-07-29.

PRIOR PILLING DATE: 2000-01-11.

PRIOR PILLING DATE: 2000-01-11.

PRIOR PILLING DATE: 2000-01-11.

PRIOR FILLING DATE: 2000-06-09.

PRIOR FILLING DATE: 2000-06-09.

NUMBER: PREDICATION NUMBER: JP 2000-241899.

PRIOR FILLING DATE: 2000-06-09.

NUMBER: PREDICATION NUMBER: JP 2000-241899.

SOFTWARE: PALENTIN VOY: 2.0.

SEQ ID NO 35.

LEAVITH: 1267.
                                                                                                                                                                                                                                                                                                                                         US-10-060-065-35; Sequence 35, Application US/10060065; Publication No. US20030017480A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jun-Ichi Yamamoto
Shizuko Ishii
Tomoyasu Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: TOShio Ota
APPLICANT: Takao Isogai
APPLICANT: Tetsuo Nishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koji Hayashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaoru Otsuka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CRGANISM: Homo sapiens
US-10-060-065-35
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Best Local Similarity
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                                                                                                                 234 STIDDFWQMVLENNSNVIAMITREIEGGIIKCYHYWPISLKKPLELKHFRVFLENYQILQ 293
                                                                                                                                                                                                                                                                     360 SAGVGRIGVFICVDVVFSAIEKNYSFDIMMIVTQMRKQRCGMIQTXEQYQFCYEIVLEVL 419
                                                                                                                                                                                                                                                                                             DFNSGNTLQNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEBYFYIATQGPLP 239
                     240 ETIEDFWONVLENNCAVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQ 299
                                                                                                                                                                              300 YFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHC 359
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100.0%; Pred. No. 1.6e-52;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE SUPPOS AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1500 & Lyon
STREET: 533 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
COUNTY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5° Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEO for Windows 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/095,478
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S-05-05-478-4
Sequence 4, Application US/09095478
Publication No. US20030095970A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
ATMAE: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/POCKET NUMBER: 224/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONS: (213) 489-1600
TELEPAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACHERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
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Best Local Similarity 100.
Matches 122; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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TOPOLOGY: lin
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us-09-095-478a-5.rapb

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APPLICANT: Franzh, Petra
APPLICANT: Appenstrum, Pontus
APPLICANT: Hellman, Ulf
Carl-Henrik
TILLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
FILE REPRENCE: L0461/7030
CURRENT APPLICATION NUMBER: US/10/177,980
CURRENT APPLICATION NUMBER: US/09/080,855
PRIOR APPLICATION NUMBER: US/09/080,855
PRIOR APPLICATION NUMBER: US/09/080,855
PRIOR APPLICATION NUMBER: US/09/080,583
PRIOR FILING DATE: 1997-02-25
SOFTWARE: FastSEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 2466
                                                                                                                                                                                                                           1067 PLPTTVGDFWOMIWEQKSTVIAMMTQBVBGEKIKCQRYWPNILGKTTMVSNRLRLALVRM 1126
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                                                                                                                                                                                                                                                                                                                                                                                                                       237 PLPETIEDFWOMVLENNCNVIAMITREIECGVIKCYSYWPISL-KBPLEPEHFSVFLETF 295
872 KMNGKLSEERTEDTDCDG----SPLPEYFTEATKMNGCEEYCEEKVKSESL----- 918
                                                             63 SDKYELVYPEPLESDTDSTVWDVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSKDT 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356 LVHCSAGVGRIGVPICVDVVFSALEXNYSPDIMNIVTONRKORCGMIQTKEQYQPCYBIV
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                                                                                                                    ----IQKPQEKKTDDDBITWG-NDELPIERTNHEDSD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/10177980; Publication No. US20030166232A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 34.7
Matches 149; Conservative
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US-10-177-980-12
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                                                      177 LPDDFNSGNTLQNRDKORPYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEBYYIATGG 236
107 LPDDFNSGNTLQNRDKORYRYIATGG 116
1013 I-----GQTKENRRKORYKNILPYDATRVPLGDEGGYINASPIKIPVGKEEFVYIACQG 1066
                                                                                                                                                                                                                        953 HSFLTNDELAVLPVVKVLPSGKYTGANLKSVIRVLRVARSGIPSKELENLOELKPLDOCL 1012
                                                                                                                                                                                                                                                                                                                                                                                                                          356 LVHCSAGVGRTGVFICVDVVFSAIBKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYBIV 415
                                                                                                                                                                                 237 PLPETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLBFEHFSVFLETF 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Yamamoto, Junichi
APPLICANT: Inhii, Shizuko
APPLICANT: Inhii, Shizuko
APPLICANT: Inhii, Shizuko
APPLICANT: Makamatu, Tomoyasu
APPLICANT: Wakamatu, Tomoyasu
APPLICANT: Wakamatu, Reiichi
APPLICANT: Wagai, Reiichi
APPLICANT: Punahashi, Shin-Ichi
APPLICANT: Funahashi, Shin-Ichi
APPLICANT: Funahashi, Shin-Ichi
APPLICANT: Benco, Chiaki
APPLICANT: Benco, Chiaki
APPLICANT: Benco, Chiaki
APPLICANT: Benco, Chiaki
APPLICANT: Bonco, Chiaki
APPLICANT: Bonco, Chiaki
APPLICANT: MOVEL GENES ENCODING PROTEIN
TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
FITLE REFERENCE: 06501-098001
CURRENT FILING DATE: 2000-01-29
PRIOR APPLICATION NUMBER: US 60/183,322
PRIOR APPLICATION NUMBER: US 60/183,532
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: UP 2000-118776
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: UP 2000-118776
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PRIOR APPLICATION NUMBER: UP 2000-118776
PRIOR FILING DATE: 2000-01-11
PRIOR SEQUICATION NUMBER: UP 2000-118776
PRIOR FILING DATE: 2000-01-11
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Publication No. US20030082776A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Ota, Toshio
APPLICANT: Isogai, Takao
APPLICANT: Isogai, Takao
APPLICANT: Hayashi, Koji
APPLICANT: Otsuka, Kaoru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1247 LYVLTRLOA 1255
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S-10-059-585-56
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APPLICANT:
APPLICANT:
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6 KVRCKTGRDNDEEEGNSGNIAMERNSLP---SSSQXMTPTKP1FGNXMNSENVKPSHHLSF 62

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Query Match 29.1%; Score 653; DB 12; Best Local Similarity 34.7%; Pred. No. 3.1e-49; Matches 149; Conservative 73; Mismatches 152;
                                                                                                                                                                                                                                               US-10-619-220-46; Application US/10619220; Publication No. US20040033979A1; GENERAL INFORMATION;
                                                                                                                                                            2464 ILYVLTRLQA 2473
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                                                                                                            415 VLEVLQNLLA 424
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ORGANISM: Homo sapiens
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APPLICANT: Marcusson, Eric G.
APPLICANT: Marcusson, Eric G.
APPLICANT: Marcusson, Eric G.
APPLICANT: Marcusson, Eric G.
APPLICANT: Marcusson, Eric G.
APPLICANT: Abrig, Hong
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE OF INVENTION: ANTISE: US/09/802,669
CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: US 09/665,615
PRIOR APPLICATION NUMBER: US 09/290,640
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 180
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 46
LENGTH: 2485
                                                                                                                                                                                                                                                                                               2135
                          :
2211 LI-----GQTKENRRKNRYKNILPYDATRVPLGDEGGYINASFIKIPVGKEEFVYIACQ 2264
                                                                                                                      136 -----IQKPQBKKTDDDEITWG-NDELPIERTWHBDSD------KD- 2169
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176 TLPDDFNSGNTLQNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHERBYFYLATQ 235
                                                                                                                                                                                                                                                                       355 LLVHCSAGVGRIGVFICVDVVFSALEXNYSPDIMNIVTQMRKQRCGMIQTKEQYQFCYEI 414
                                                                                      236 GPLPETIEDFWOMVLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLET 294
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                                                                                                                                                                             295 PHVTQYPTVRVPQIVKKSTGKSQCVKHLQFTKWPDHGTPASADPPIKYVRKYHRGP
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Patent No. US20020004490A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         2445 ILYVLTRLOA 2454
                                                                                                                                                                                                                                                                                                                                                              415 VLEVLONLLA 424
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ORGANISM: Homo sapiens
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PAPPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
APPLICANT: Chang, Hong
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REPRESENCE: 128PH-545
FILE REPRESENCE: 128PH-545
FILE REPRESENCE: 1290-07-14
FILE PRICA PLICATION NUMBER: 09/665,615
FILE REPRESENCE: 2001-03-01
FILE PRICA PLICATION NUMBER: 09/665,615
FILE REPRESENCE: 2000-09-18
FILE PRICA PLICATION NUMBER: US 09/665,615
FILE PRICA PLICATION NUMBER: US 09/290,640
                                                                                                                                                                                                                                                                           2344 MQQLKGEVVRAMTLEDIQTRBVRHISHLNFTAWPDHDTPSQPDDLLTPISYMRHIHRSGP 2403
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                                                                                                                                                                                                                               APPLICANT: 2xang, Bing
APPLICANT: Chang, Bradford W. APPLICANT: Gibson, Bradford W. APPLICANT: Taylor, Steven W. APPLICANT: Taylor, Steven W. APPLICANT: Glenn, Gary W. APPLICANT: Marnock, Dale B. TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME FILE REPRENCE: 660084.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT PILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: Factor DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: Factor Windows Version 4.0
SEQ ID NO 1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56
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Sequence 1349, Application US/10408765A Publication No. US20040101874A1 GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Pahy, Boin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USCULT 14
IS-09-095-478-7
Sequence 7, Application US/09095478
Publication No. US20030095970A1
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :| || | |
2464 ILYVLTRLQA 2473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S-10-408-765A-1349
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Gregory NOVEL PROTEIN TYROSINE PHOSPHATASE SUPTPOS AND RELATED PRODUCTS AND

> TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:

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71 PEPL-----ESDTDETVWDVS-----DRSLRNRWNSMD-SETAGPSKTVSPVLSGS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 NASYIRIVNHEEBYFYIATOGPLPETIEDFWOMYLENNCNVIAMITREIECGVIKCYSYW 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292 QPDDLLTFISYWRHIRRS---GPVITHCSAGIGRSGTLICIDVVLGLISQDLEFDISDLV 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 SRLSKD--TETS-----VSEKELTQLAQIRPLIFNSSARSAMRDCLNTLQ---- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 ---KKBELDIIREFLELEGMTLPDDFNSGNTLQNRDKNRYRDILPYDSTRVPLGKNKDYI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 PISL-KEPLEFEHPSVPLETFHVTQYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 PSILGTTTWANERLRLALLRMQQLKGFIVRVWALEDIQTGEVRHISHLNFTAWPDHDTPS 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335 SAD---PRIKYVRYVRYSHITGPLLVHCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIV 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 28.8%; Score 644.5; DB 10; Length 381; Best Local Similarity 38.4%; Pred. No. 1.2e-49; Matches 151; Conservative 66; Mismatches 125; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392 TOWRKORCGMIQTKEQYQFCYRIVLEVLONLLA 424
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                                                                ADDRESSEE: Lyon & Lyon STREET: 637 West Pitch Street STREET: 631 West Pitch Street STREET: 631 West Pitch Street STREET: 03.1c 4700 CITY: Los Angeles STATE: California COUNTRY: U.S.A. ZIP: 90071-2066 COMPUTES READABLE FORM: MEDIUM TYPE: storage MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Fast SEQ for Windows 2.0
CURRENT APPLICATION NUMBER: US/09/095,478
FILING DATE:
RECASIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PRIOR APPLICATION DATA:
PRIOR DATE:
PRING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY CASH INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEX: 67-3510
INFORMATION POS SEQ ID NO: 7:
SEGUREC GRARACTERISTICS:
LENGTH: 381 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 381 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPCLOGY: linear
MOLECULE TYPE: Peptide
                    NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
FITLE OF INVENTION:
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        Qy
        329 DHGTPASADFTKYVRYVRKSHITGPLAVHCSAGVGRTGVDVVFSAIEKNYSFDIM 388

        Db
        263 DHDTPSQPDDLLTFISYMRHIHRSGPIITHCSAGIGRSGTLICIDVVLGLISQDLDFDIS 322

        Qy
        389 NIVTQMRKQRCAMICHERQYGFCYTIVLEVLQNLLA 424

        Db
        323 DLVRCMRLQRHGMVQTEDQYIFCYQVILYULRLQA 358

        Search completed: June 16, 2004, 13:30:18

        Job time : 50 secs
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5

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protein-tyrosine-phosphatase homolog DKFZp566K0524.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: il-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C;Accession: T08716
R;Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Accession: T08716
A;Coss-references: ExBL:AloSo040
A;Experimental source: fetal kidney; clone DKFZp566K0524
C;Genefics:
A;Note: DKFZp566K0524.1
C;Superfamily: protein-tyrosine-phosphatase homology
F;161-379/Domain: protein-tyrosine-phosphatase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 ETAGPSKTVSPVLSGSSRLSKDTETSVSEKELTQLAQIRPLIPNSSARSAMRDCLNTLQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKEPLEFEHFSVFLETFHVTQY FTVRVFQI VKKSTGKSQCVKHLQFTKWPDHGTPASADF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.5%; Score 1310; DB 2; Length 398; 65.4%; Pred. No. 2.4e-87; ive 48; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
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A48066
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TDHULK
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A16710
A46151
A461151
A46151
A4
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Best Local Similarity 65.4%
Watches 253; Conservative
     582
11457
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11405
11168
12168
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Copyright (c) 1993 - 2004 Compugen Ltd.
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protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 3 - 1 c/species: Homo sapiens (man) C/species: 129-May-1998 #text_change 30-Jun-2002 C/sAccession: 167630 B/Maekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S. Rimaekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S. Rimaekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S. Rimaekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S. A; Tile: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane A; Reference number: 153483; MuID:94116679; PIDN:BASP1977 A; Rolecule type: mRNA A; Residues: 1-2549 - RESS A; Residues: 1-2549 - RESS C; Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology; C; Reywords: phosphata: monoseker hydrolase P; 574-8681/Domain: protein 4.1 membrane-binding domain homology <B41> F; 182-1256/Domain: protein-tyrosine-phosphatase homology <PTP> F; 182-1256/Domain: protein-tyrosine-phosphatase homology <PTP>
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Best Local Similarity 34.7%; Pred. No. 1.2e-38;
Matches 149; Conservative 73; Mismatches 152; Indels 5:
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;Cross-references: GB:134581; NID:9806295; PIDN:AAC42055.1; PID:9806296
;Hendriks, W.; Brugman, C.; Zeeuwen, F.; Schepens, J.; Wieringa, B.
ubmitted to the EMBL Data Library, Jume 1993
;Description: Assessment of the expression levels of murine protein-tyrosine phosphatas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Map position: 5
'Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGP domain homology;
'Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGP domain homology;
'Reywords: phosphoprotein, phosphoric monoester hydrolase; transmembrane protein; tyros
'566-860/Domain: protein 4.1 membrane-binding domain homology scLG1>
'1369-1165/Domain: GLGF domain homology scLG3>
'1459-1840/Domain: GLGF domain homology scLG3>
'1459-1840/Domain: GLGF domain homology scLG3>
'1459-1840/Domain: GLGF domain homology scLG3>
'1303-1937/Domain: protein-tyrosine-phosphatase homology spTP1>
'2303-2422/Domain: protein-tyrosine-phosphatase homology scRG3>
'2314/Active site: Cys (phosphocysteine intermediate) #status predicted
'2380/Binding site: substrate phosphate (Arg) #status predicted
                                                           rotein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 13 - mouse
Alternate names: epidernal growth factor-binding protein; serine proteinase
Species: Mus musculus (house mouse)
Date: 27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 21-Jun-2002
Accession: 871825; 867987; IB1210; IB1209; 840290
CES Lett. 358, 233-239, 1995
ERS Lett. 358, 233-239, 1995
FILLE: Characterization of a protein tyrosine phosphatase (RIP) expressed at a very ea
Recession: 871625; MUID:95145716; PMID:7843407
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;Residues: 1-2450 cCHI>
;Cross-references: EMBi:D83966; NID:g1232103; PIDN:BAA12158.1; PID:g1232104
;Experimental source: strain DBA/2; cell line MEL 745A
;Molf, B.B.; Brown, M.D.
EBS Lett. 376, 177-180, 1995
;Title: Epidermal growth factor-binding protein activates soluble and receptor-bound *
;Reference number: S67987; MUID:96105375; PMID:7498536
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.Residues: 2266-2372 <HEN>
:Cross-references: EMBL:223059; NID:g438155; PIDN:CAA80594.1; PID:g438156
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Residues: 1090-1102 <#MOLD.
Residues: 1090-1102 <#MOLD.
Residues: 1090-1102 <#MOLD.
Tarie, S.; Kitada, S.; Reed, J.C.
Cience 268, 411-415, 1995
Title: RAP-11 a protein tyrosine phosphatase that associates with Fas.
Reference number: 159595; MUID:95232528; PMID:7536343
Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: mRNA
Residues: 1259-1354, K',1356-1447, R',1449-1454 <RES>
Cross-references: GB:L34582; NID:g806297; PIDN:AAC42056.1; PID:g806298
Accession: 181209
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iive 75; Mismatches 154; Indels 120;
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167; Conservative
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protein-tyrosine-phosphatase (BC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 1 [viral protein-tyrosine-phosphatase FAP-1; protein-tyrosine-phosphatase hPTPLE C.Species: Homo sapiens (man) c.Species: 11-Nov-1994 #sequence revision 08-Feb-1996 #text_change 21-Jun-2002 c.Accession: A54971; A55114; I59595; I53483; S46955 Figuralle, S. Shad, S.; Stocco, R.; Shen, S.H. J. Ahmad, S.; Stocco, R.; Shen, S.H. J. Ahmad, S.; Stocco, R.; Shen, S.H. Ayritle: A novel protein-tyrosine phosphatase with homology to both the cytoskeletal protein-tyrosine phosphatase with 
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C; Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology; J C; Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology; J C; Stewardse alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyrosin F; 574-868/Domain: protein 4.1 membrane-binding domain homology <GLG1>
F; 1973-454/Domain: GLGF domain homology <GLG2>
F; 1973-454/Domain: GLGF domain homology <GLG3>
F; 1979-1870/Domain: GLGF domain homology <GLG3>
F; 1993-1967/Domain: GLGF domain homology <GLG3>
F; 1993-1967/Domain: GLGF domain homology <GLG5>
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A.Molecule type: mRNA
A.Molecule type: mRNA
A.Forsidues: 1-2490 «BAN»
A.Cross-references: GB:U12128
A.Note: sequence shown follows authors' translation at positions 62-63
B.Asaras, J.; Claesson-Welsh, L.; Heldin, C.H.; Gonez, L.J.
J. Biol. Chem. 269, 24082-24089, 1994
A.Fitle: Cloning and characterization of PTPL1, a protein tyrosine phosphatase with simi.
A.Reference number: A55114; WUID:95014139; PMID:7929060
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A; Mosdicuse: 1.61, 68. 64-839, 'D', 841-1055, 1075-1133,'FH', 1136-1210,'I', 1212-1383,1389-15.
A; Cross-references: GB: 880289; NID: 9515030; PIDN: CAA56563.1; PID: 9515031
R; Sato, T.; Irie, S.; Kitada, S.; Reed, J.C.
R; Science 268, 411-415, 1995
A; Title: PAP-1: a protein tyrosine phosphatase that associates with Fas.
A; Reference number: 159595; MUID: 95232528; PMID: 7536343
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R;Maekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
BSBS Lett. 337, 200-206; 1994
A;Title: Molecular Coloning of a movel protein-tyrosine phosphatase containing a membrane-A;Reference number: 153483; MUID:94116679; PMID:8287977
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A;Cross-references: GB:D21209; NID:g452189; PIDN:BAA04750.1; PID:g452190
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F;2413/Active site: Cys (phosphocysteine intermediate) #status predicted
F;2419/Binding site: substrate phosphate (Arg) #status predicted
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A;Molecule type: mRNA
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A;Molecule type: mRNA
A;Residues: 1279-1888 <RES>
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ISS Left. 137, 200-206, 1994
Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane
Reference number: 153483; MUID:94116679; PMID:8287977
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Cross-references: GB:D21210; NID:g452191; PIDN:BAA04751.1; PID:g452192
Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;
Keywords: phosphoric monoester hydrolase
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, Molecule type: mRNA, Residues: 1-913 < YAN>, Itchs. F.; Hinoda, Y.; Toyota, M.; Makiguchi, Y.; Imai, K.; Yachi, A. Gastroenterol. 29, 727-732, 1994

"Athle: Expression of cytoskeletal-associated protein tyrosine phosphatase PTPHI mRNA in Reference number: 155698; MUID:99179278; PMID:7874267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 27-Mar-1992 #sequence_revision 02-May-1994 #text_change 21-Jun-2002
C;Accession: A41109; 155698
C;Accession: A41109; 155698
R;Yang, Q;? Tonks, N.K.
Proc. Natl. Acad. Sci. U.S.A. 88, 5949-5953, 1991
A;Title: Isolation of a cDNA clone encoding a human protein-tyrosine phosphatase with hom A;Reference number: A41109; MUID:91296738; PMID:1648725
A;Accession: A41109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN3, nonreceptor type 3 [validated] N;Alternate names: PTPH1
                                                                                              988 HTCHDFWOWWEQGVNVIAMVTAEEEGGRTKSHRYWP----KLGSKHSSATYGKFKVTT 1042
                                                                                                                                                                                                                               1003 KF--RTDSVCYATTGLKVKHLLSGQERTVWHLQYTDWPDHGCPEDVQGFLSYLEEIQSVR 1100
                                                                                                                                                                                                                                                                                                                                        15;
                                  240 ETIEDFWOMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEPEHFSVPLETFHVTQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               345 YVRKSHITG-----PLLVHCSAGVGRTGVFICVDVVFSAIEKNYSPDIMNIVTQMRKQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 RDNDEBEGNSGNIANIRNSIPSSSQKMTPTKPIFGNKMNSENVKPS--HHLSFSDKYELVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 PEPLESDTDETVWDVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSKDTETSVSEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   564 GRDISEHTHDOV------VMFIKASRESHSRELALVIRRRAVRSFADPKSEDE
                                                                                                                                                                300 YFTVRVFQIVKKST-----GKSQCVKHLQFTKWPDHGTPASADPFIKY----VR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 LPDDFNSGNTLQNRDKARYRDILPYDSTRVPLGKAKDYINASYI------RIVNHBEEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Status: translated from GB/EMBL/DDBJ
A,Modecule type: mRNA
A,Residues: 899-913 <RES-
A,Cross-references: GB:S76309; NID:g913165; PIDN:AAB33583.1; PID:g913166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTQLAQIRPLIFNSSARSAMRDCL--NTLQXKEELDIIREFLELEQM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Cross-references: GDB:131386; OMIM:176877
A, Map position: 9q31-9q31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1161 MFMIQTIAQYKFVYQVLIQFLQN 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                399 CGMIQTKEQYOFCYEIVLEVLON 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene: GDB: PTPN3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith, A.L.; Mitchell, P.J.; Shipley, J.; Gusterson, B.A.; Rogers, M.V.; Crompton, M.F. iochem. Blophys. Res. Commun. 209, 959-965, 1995. Fittle: PEz:a novel human cDNA encoding protein tyrosine phosphatase-and ezrin-like dom Reference number: JC4155; MUID:95251727; PMID:7733990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Cross-references: GDB.454485
;Map possition: 1942.2-1942.2
;Map possition: 1942.2-1942.2
;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-b; Keywords: phosphoprotein, phosphoric monoester hydrolase; tyrosine-specific phosphatas; 5.23-30.70main: protein 4.1 membrane-binding domain homology <B41>
;566-575/Region: acidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rotein-tyrosine-phosphatase (BC 3.1.3.48), nonreceptor type 14 - human Alternate names: PEZ protein; protein-tyrosine-phosphatase/ezrin-like protein; Species: Homo sapiens (man); Species: Homo sapiens (man); Date: 27-Aug-1995 #sequence_revision 23-Feb-1996 #text_change 21-Jul-2000; Accession: JC4155
                                                                                                                                                                                                                                                                                                                                                                                                                                       2409 IITHCSAGIGRSGTLICIDVVLGLISQDLDFDISDLYRCWRLQRHGWVQTBDQYIFCYQV 2468
                                                                                                                                                                           2349 MQQLKGFVVRAMTLEDIQTREVRHISHLNFTAWPDHDTPSQPDDLLIFISYMRHIHRSGP 2408
                                         LLVHCSAGVGRTGVFICVDVVFSAIBKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEI 414
                                                                                                                                                                                                                                                                  FHVTQYPTVRVFQIVKKSTGKSQCVKHLQPTKWPDHGTPASADFPIKYVRYVRKSHITGP 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----EEAPESVPQIPMLREKWEYSAQLQAALARIPNKPPPEYPGP 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----AQIRPLEP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 TLPDDFNSGNTLQNRDKNRYRDILPRYDSTRVPLGKOKKDYINASYIRIVNHEBEXFFYLATQ 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          808 ISEPDLISVKERVKKEPVKERPVSEMFSLEDSIIEREMMIRNLEKOKMAGLEAOKRPLML 867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 GNTLONRDKNRYRDILPYDSTRVPL----GKNKDYINASYIRIVNHEEEYFYIATQGPLP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :Molecule type: mRNA
:Residues: 1-1187 <SMI>
:Cross-references: EMBL:X82676; NID:g3929753; PIDN:CAA57993.1; PID:g809029
                                                                                                                                    236 GPLPETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISL-KBPLEFEHFSVFLET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,933-1169/Domain: protein-tyrosine-phosphatase homology <PTP2>
,1121/Active site: Cys (phosphocysteine intermediate) #status predicted
,1127/Binding site: substrate phosphate (Arg) #status predicted
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30.0%; Pred. No. 1.3e-29;
iive 73; Mismatches 156
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2469 ILYVLTRLQA 2478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLEVLONLLA 424
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Matches
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Db 984 TQCPLPHTCHDFWQWWBQCVNVIAMVTABEBCGRTKSHRYWPKLGSKHSSATYG 1038 Qy 294 TFHVTQYPTVRVPQIVKSTGKSQCYKHLQFTKWPDHGTPAADFFIKY 342	es: ty	S; Conservat KMTPTKEIFGNK KHTGSVDIYGH- MDSETAGPSKTV H LQKKEBLDIIRE	212 KDYINASYIRIVNHEBEYFYIATOGPLPETIEDPWQWVLENNCNYLAMITRELECGVIKC 271 1836 SDYINASYIRIVNHEBEYFYIATOGPLPETIEDPWQWVLENNCNYLAMITRELECGVIKC 271 1836 SDYINASPID-GYRKRAYIATOGPLPETIEDPWQRVLENNCNYLAMITRELECGVIKC 271 272 KSYWPISLKRPLEFEHPSVF-LEFFFYVTOYFYTWRVGIVKKSTGKSQCVKHLQFTKWPDH 330 1	Oy 387 IMMIVTOMERORGENIOTREQUECTEIVLEVI. 419
Y 230 FYIATQGPLPETIEDFWGWLERNCNVIAMITRELECGVIKCYSYWPISLKEPLEFEH 287	SSULT 8 2346 Cotein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 14 - mouse Alternate names: PEZ protein, protein-tyrosine-phosphatase PTP36; protein-tyrosine-phosphates: PED forces: Muss musculus (house mouse) Date: 24-Feb-1995 #sequence_revision 23-Feb-1996 #text_change 21-Jul-2000 Date: 24-Feb-1995 #sequence_revision 23-Feb-1996 #text_change 21-Jul-2000 Sawada, M.; Ogata, M.; Fujino, Y.; Hamaoka, T. Lochem. Blopbys. Res. Commun. 203, 479-484, 1994 Title: CDNA cloning of a novel protein tyrosine phosphatase with homology to cytoskele Residues: Unit 202366 Molecule type: mRNA Residues: 1-1189 <-AAMA Cross-references: GB:331842; NID:9507330; PIDN:BAA06628.1; PID:9507331 Experimental source: thymus Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-bisphatase; typosine-specific phosphatase 23-302/pomain: protein 4.1 membrane-binding domain homology k841>	566-575/Region: proline-rich 712-718/Region: acidic 935-1171/Domain: acidic 920-1171/Domain: acidic 935-1171/Domain: acidic 93	56 PSHH-LEFSDXYELVYPEPLESDTDETVMDVSDR	141 IFNSSARSAMRDCLATLQKKESLDIIREFLELEQMTLPDD 180 168 MLAALNGLSVARVSGREDGRHDATRVPIDERLRALKKKLEDGMVFTEYEQIPNKKA 923 181FNSGNTLQNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEESYFYIA 233 182FNSGNTLQNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEESYFYIA 233 234 NGVFSTATLFRANGKYPERRVELIPTKENNYGYINASHIKVVVGGSSHHYIA 983 234 TQGPLPETIEDFWQWYLENNCAVIAMITRSIECGVIKCYSYWPISLKEPLEFEHFSVFLE 293 [

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Cipaces 10-Apression: $51005; S5160.

Cipacession: $51005; S5161.

Ril'Abbe, D.; Banville, D.; Tong, Y.; Stocco, R.; Masson, S.; Ma, S.; Fantus, G.; Shen, FBBS Lett. 356, 131-356, 1934

A; Title: Identification of a novel protein tyrosine phosphatase with sequence homology to A; Reference number: $51005; MUID:95104449; PMID:7805871

A; Reference number: $51005

A; Reference number: $51005

A; Residues: 1-1175 < LAA>

A; Cross-references: EMBL:U17971; NID:9662113; PIDN:AAA62153.1; PID:9602255

A; Residues: PTPZE

A; Residues: B40-1175 < LAB>
A; Residues: B40-1175 < LAB>
A; Cross-references: EMBL:U18293; NID:9603228; PIDN:AAA62154.1; PID:9603229

A; Residues: B40-1175 < LAB>
A; Cross-references: EMBL:U18293; NID:9603228; PIDN:AAA62154.1; PID:9603229

A; Genetics: PTPZE

C; Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 PRLIFARESQEQQLNYPCASVTPVTGPLHIFEPKSHVTEPEKRAKDISPVHLVMETHQPRR 789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             900 EYERILKCRLVDGECSTARLPENAERNRFQDVLPYDDARVELVPTKENNTGYINASHIKV 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 VNHESEYFYIATQGPLPETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEP 282
                                                                                   protein-tyrosine-phosphatase (EC 3.1.3.48) 2E - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Apr-1996 #sequence_revision 03-May-1996 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 IPGNYANSENVKP-----SHHLSPSDKYELVYPEPLESDTDETVWDVSDRSLRNRWNSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------OTLN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----QNRDKNRYRDILPYDSTRVPLGKNKD----YINASYIRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         960 SVSGIEWDYJATOGPLONTCODFWOWWEQCVALIAWVTAEEEGGREKSFRYWP----R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283 LEFEHRSVFLETFHVTQYF----TVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 336 ADFFIKYVRYV----RKSHITG------PLLVHCSAGVGRIGVFICVDVVFSAIEKNYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --LSGSSRLSKD-----TET-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.6%; Score 484.5; DB 2; Length 1175; 28.2%; Pred. No. 7.5e-27; cive 69; Mismatches 141; Indels 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 -KKBELDIIR-----EFLELEOMILPODFNSGWIL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1135 LDIPRVLELLRQQRMMLVQTLSQYTFVYRVLIQFLKS 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDIMNIVIOMRKORCGMIQTKEQYQFCYBIVLEVLON 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SVSEKELTQLAQIRPLIFNSSARSAMRDCL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 28.2
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 DSETAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Honda, H.; Inazawa, J.; Nishida, J.; Yazaki, Y.; Hirai, H.

lood 84, 4186-4194, 1994

Title: Molecular cloning, characterization, and chromosomal localization of a novel printer molecular cloning, characterization, and chromosomal localization of a novel printer molecular cloning, translated from GB/EMBL/DDBJ

Status: preliminary; translated from GB/EMBL/DDBJ

Molecule type: mRNA

Residues: 1-216, LTGVRKAA,,225-260,'G',262-285,'GTEGGLDASNTERSBA',302,'S',304,'TAPVHDB

Cross-references: GB:D37781; NID:g633072; PIDN:BAA07035.1; PID:g633073

Comment: Enhanced expression of this protein with increasing cell density suggests a reconstruction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Bescription: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine and 'Superfamily: protein-tyrosine-phosphatase, receptor type j; fibronectin type III repea 'Reywords: glycoprotein; phosphoric monoester hydrolase; receptor; tran. 1.35/Domain: signal sequence #status predicted <SIG. 1337/Product: protein-tyrosine-phosphatase, receptor type J #status predicted <MAT>:18-197/Domain: fibronectin type III repeat homology <3FNA>:206-283/Domain: fibronectin type III repeat homology #status atypical <3FNC>:365-445/Domain: fibronectin type III repeat homology %3FND>:355-445/Domain: fibronectin type III repeat homology <3FND>:355-417/Domain: fibronectin type III repeat homology <3FNB>:353-617/Domain: fibronectin type III repeat homology <3FNB>:720-2804/Domain: fibronectin type III repeat homology <3FNB>:720-804/Domain: fibronectin type III repeat homology <3FNB>:720-808/Domain: fibronectin type III repeat homology <70-808/Domain: fibron
                                                                                                                                                                                     enhanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;1065-1287/Domain: protein-tyrosine-phosphatase homology <PTP>
;72,82,33,104,142,172,192,231,288,278,342,351,376,393,396,413,431,501,525,536,582,603,
;1239/Active site: Cys (phosphocysteine intermediate) #status predicted
;1245/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1109 PIATQGPLPNTLKDFWRMVWEKNVYAIIMLTKCVBQGRTKCESYWP--SKQAQDYGDITV 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1227 KOSPPESPILVHCSAGVGRTGTFIAIDRLIYQIENENTVDVYGIVYDLRMHRPLMVQTED 1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 SKDTETSVSEKELTQLAQIRPLIFNSSARSAMRDCLNTLQKKEELD----IIREFLELEQ 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 MTLPDDFNSGNTLQNRDKNRYRDILPYDSTRVPLG----KNKDYINASYIRIVNHEEEYF 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 FLETFHVTQYFTVRVPQIVKKSTGKSQCVNHLQFTKWPDHGTPASADFFIKY---VR-YV 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347 RKSHITGPLLVHCSAGVGRTGVFICVDVVFSALEKNYSFDIMNIVTQMRKQRCGMIQTKE 406
Date: 01-Mar-1996 #sequence_revision 08-Mar-1996 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YIATQGPLPETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEPEHFSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.7%; Score 487; DB 1; Length 13 34.9%; Pred. No. 6e-27; ive 63; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                .Molecule type: mRNA
.Residues: 1-1337 <RES>
.Cross-references: EMBL:U10886; NID:g558754; PID:g558755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: GDB:385040; OMIM:600925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || | : ||::::
QYVFLNQCVLDIVRS 1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Experimental source: HeLa cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Map position: 19q13.4-19q13.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 110; Conservative
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27 Q. 2 Ω. > Ω > Д 12

RESULT

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A; Title: Structural diversity and evolution of human receptor-like protein tyrosine phoses A; Reference number: S12049; MUID:91006018; PMID:2170109
A; Accession: S12052
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 390-1912 (xRU-)
A; Note: the sequence from Fig. 5B is inconsistent with that from Fig. 5A in having 568-T
B; Adadhi, M.; Sekiya, M.; Arianra, Y.; Takekawa, M.; Itoh, F.; Hinoda, Y.; Imai, K.; Yac
Cancer Res. 52, 77-740, 1992
A; Note: the sequence from Fig. 5B is inconsistent with that from Fig. 5A in having 568-T
R; Adacer Res. 52, 77-740, 1992
A; Note: the sequence from Fig. 5B is inconsistent with that from Fig. 5A in having 568-T
A; Reference number: A44929; MUID:92119637; PMID:1370651
A; Recession: B44929
A; Molecule type: mRNA
A; Residues: 1756-1804, CC, 1806-1845 <ADA->
A; Cross-references: GB:S78086; NID:9243345; PIDN:AAB21147.1; PID:9243546
A; Reperimental source: pre-B cell NALM-6
A; Reperimental source: gre-B cell NALM-6
A; Note: the authors did not report the entire codon for residue 90
C; Genetics:
A; Map position: 924-924
A; Map position: 924-924
A; Map position: 924-924
C; Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein tyrosine phosphatase - mouse
(Species: Ms musculus (house mouse)
(Species: Ms musculus (house mouse)
(Species: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 22-Jun-1999
(Species: ISB345 #sequence_revision 26-Jul-1996 #text_change 22-Jun-1999
(Shigrashistuji, H; Aili, S.; Purutani, M.; Imamura, M.; Kaneko, Y.; Takenawa, J.; Nakaya
(Oncogene 10, 407-414, 1995
A;Title: Enhanced expression of multiple protein tyrosine phosphatases in the regeneratir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C,Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane | F;88-100/Domain: immunoglobulin homology <IMM1> | F;40-209/Domain: immunoglobulin homology <IMM2> | F;40-209/Domain: immunoglobulin homology <IMM3> | F;250-304/Domain: immunoglobulin homology <IMM3> | F;211-811/Domain: immunoglobulin homology <IMM3> | F;711-811/Domain: immunoglobulin homology <IMM3> | F;711-811/Domain: ibronectin type III repeat homology <3FR> | F;11293-1912/Domain: ibronectin type III repeat homology <PFP2> | F;1531/Active site: Cys (phosphocysteine intermediate #status predicted | F;1531/Active site: Cys (phosphocysteine intermediate) #status predicted | F;1844/Active site: Cys (phosphocysteine intermediate) #status predicted | F;1850/Binding site: substrate phosphate (Arg) #status predicted | F;1850/Binding site: substrate phosphate (Arg) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 LELEQMTLPDD-----FNSGNTLQNRDKNRYRDILPYDSTRVPLG----KNKDYINAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1644 MELEFKRLASSKAHTSRFISANLPCNKFKNRLVNIMPYESTRVCLQPIRGVEGSDYINAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279 LKEPLEFZHPSVF-LETFHVTQYFTVRVPQIVKKSTGKSQCVKHLQPTKWPDHGTPASAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIKYVRYVRKSH----ITGPLLVHCSAGVGRTGVFICVDVVFSALEKNYSFDIMNIVTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 1912;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tal protein 4.1.
A;Reference number: I58345; MJID:95140431; PMID:7838537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394 MRKQRCGMIQTXEQYQFCYEIVLEVL 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 40.2%
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas; 148-208f/Domain: immunoglobulin homology <1MM1>
148-299f/Domain: immunoglobulin homology <1MM1>
1317-399f/Domain: immunoglobulin homology <1MM2>
1317-399f/Domain: immunoglobulin homology <1RR>
1317-399f/Domain: fibronectin type III repeat homology <3FR>
1317-399f/Domain: procein-type III repeat homology <1RE>
1317-3479f/Domain: procein-tyrosine-phosphatase homology <PTP2>
13147f/Active site: Cys (phosphocysteine intermediate) #status predicted
1322f/Active site: Cys (phosphocysteine intermediate) #status predicted
1438/Binding site: substrate phosphate (Arg) #status predicted
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Alternate names: protein-tyrosine-phosphatase BPTP-2
Species: Homo sapiens (man)
Bayecies: Headrance revision 03-0ct-1995 #text_change 21-Jan-2000
Accession: A56178; S12052; B44929
Phildo, R.; Krueger, N.X.; Serra-Pages, C.; Saito, H.; Streuli, M.
Baid: Chem. 270, 6722-6728, 1995
Filtle: Molecular characterization of the human transmembrane protein-tyrosine phosphat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
                                                                                                                                                                                               Stoker, A.W.
ech. Dev. 46, 201-217, 1994
,Title: Isoforms of a novel cell adhesion molecule-like protein tyrosine phosphatase ,Reference number: ISO212; MUID:95001563; PMID:7918104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1329 VMLTKLREMGREKCHQYWP--AERSARYQYFVVDPMAEYNWPQYI-LREFKVTDARDGQS 1385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 RDCLNTLQKKEBELDIIREF--LELZQMTLPDD-----FNSGNTLQNRDKNRYRDILPYD 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRVPLG-----KNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQMVLENNCNVI 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317 QCVKHLQFTKMPDHGTPASADFFIKYVRYVRKSH----ITGPLLVHCSAGVGRTGVFICV 372
                                                                                     .Species: Gallus gallus (chicken)
Jobe: 1. Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
Accession: IS0212
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                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: mRNA
Residues: 1-1499 <STO>
:Cross-references: GB:L32780; NID:g485746; PIDN:AAA64460.1; PID:g485747
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;Molecule type: mRNA
;Residues: 1-1912 <PUL.>
;Cross-references: GB-L38929; NID:g755652; PIDN:AAC41749.1; PID:g755653
;Krueger, N.X.; Streuli, M.; Saito, H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.6%; Score 483; DB 2; Length 149
38.0%; Pred. No. 1.4e-26;
Live 54; Mismatches 100; Indels
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    chicken

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                                                         rotein-tyrosine-phosphatase (EC 3.1.3.48)
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109, Conservative
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Accession: I58345

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                                                                                                                                                                 Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-phosphoprotein

Keywords: phosphoprotein

225-304/Domain: protein 4.1 membrane-binding domain homology < 2841>
225-304/Domain: protein-tyrosine-phosphatase homology < PTP2>

1110/Active site: Cys (phosphocysteine intermediate) #status predicted

1116/Binding site: substrate phosphate (Arg) #status predicted
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Biol. Chem. 269, 19639-19645, 1994
Fitle: Characterization of two structurally related Xenopus laevis protein tyrosine ph. Reference number: A53978; MUID:94308257; PMID:8034733
Accession: B53978
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;Species: Xenopus laevis (African clawed frog)
;Date: 25-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Note: sequence extracted from NCBI backbone (NCBIN:149759, NCBIP:149760)
:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 9; cellular retinaldehyde-
                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          677 VFSDKWKQEGTEEQEGGRYSHKKSLSDATMLIDSSEEDEDLEEDSSREQAISAVSEPRLT 736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----KSHITGPLLVHCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRC 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 IPGNKONSENVKP----SHHLSFSDKYELV----YPEPLESDT--DETVWDVSDRSLR
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
o;Status: preliminary; translated from objectus, constitution type: mRNA; Molecule type: mRNA;;Residues: 1-1176 <RES>;;Cross-references: GB:D37801; NID:g604885; PIDN:BAA07053.1; PID:g604886
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                                                                                                                                                                                                                                                                                                                                                                               21.5%; Score 481; DB 2; Length 1176; 28.5%; Pred. No. 1.3e-26; tive 74; Mismatches 155; Indels 130;
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1151 MLVQTLGQYTFVYRVLIQFLKS 1172
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                                                                                                                                                                                                                                                                                                                                                                                                                                          143; Conservative
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Residues: 1-597 <DEL>
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                                                                                                                                               Gene: PTP-RL10
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Best Local (
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monoester hydrolase; tyrosine-specific phosphatas
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                                                                                                                                                                                                                                                                                                                                                                                                                152 DCLNTLQKKEBLDIIREFLELEGMTLPDDFNSGNTLQNRDKNRYRDILPYDSTRVPLG-- 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         409 GRIKCGOYWPLEAGRSEDTGHF--IIRNIHIDLFQDFKLTHFEVYNKOTDESRSVAHYQY 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325 TKWPDHGTPASADPPIKYVRYVRK-----SHITG-PLLVHCSAGVGRTGVF 369
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                                       F.38-227/Domain: cellular retinaldehyde-binding protein homology <CRB>F.328-564/Domain: protein-tyrosine-phosphatase homology <FP>F.516-F.516/Active site: Cys (bhosphocysteine intermediate) #status predicter F.516/Active site: gubstrate phosphate (Arg) #status predicter F.522/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             370 ICVDVVFSAIEKNYSPDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ 420
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                                                                                                                                                                                                                                           Query Match 21.4%; Score 479; DB 2; Length 597; Best Local Similarity 35.7%; Pred. No. 6.9e-27; Matches 104; Conservative 51; Mismatches 110; Indels
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us-09-095-478a-5.rsp

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SEQUENCE FROM N.A.
TISSUB-Fibroblast;
MEDLINE-SS014139; PubMed=7929060;
Saras J., Claesson-Welsh L., Heldin C.-H., Gonez L.J.;
Gloning and characterization of PTPL1, a protein tyrosine phosphatase with similarities to cytoskeletal-associated proteins.";
J. Biol. Chem. 269:24082-24089(1994).
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MEDINE-94116679; PubMed-8287977;

Mackawa X., Imagawa N., Nagamatsu M., Harada S.;

Molecular Cloning of a novel protein-tyrosine phosphatase containing a membrane-binding domain and GLGF repeats.";

FESS Lett. 337:200-206(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95232528; PubMed-7536343;
Sato T., Irie S., Kitada S., Reed J.C.;
"FAD-1: a protein tyrosine phosphatase that associates with Fas.";
Science 268:411-415(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang H.Y.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1279-1883 FROM N.A. (ISOFORM 4)
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TISSUE=Pancreas;
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Q1332 homo sapien
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P17706 homo sapien
P17706 homo sapien
Q1687 homo sapien
                                                                                                     June 16, 2004, 13:16:50 ; Search time 17 Seconds (without alignments) 1304.817 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 GNTLONRDKARYRDILPYDSTRVPL----GKNKDYINASYIRIVNHEEBYFYIATQGPLP
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                                                                                                                                                                  MIM: 603155; -.

GO: GO:0064725; F:protein tyrosine phosphatase activity; TAS
GO: GO:0006470; P:protein amino acid dephosphorylation; TAS.
InterPro: IPR000299; Band 4.1.
InterPro: IPR000387; TYR_phosphatase.
InterPro: IPR000387; TYR_phosphatase.
Pfam: PF00731; Band 41; 1.

Pfam: PF00102; Y_phosphatase; 1.

PRINTS; PR001035; BAND41.

PRINTS; PR00195; BALD41.
SMART; SM00199; PTPC: 1.
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PROSITE; PSOOGEG; PERM 1; 1.

PROSITE; PSOOGEG; PERM 2; 1.

ROSITE; PSOOGE7; PERM 3; 1.

R PROSITE; PSOOGE7; PTR PHOSPHATASE 1; 1.

R PROSITE; PSOOGE5; TYR PHOSPHATASE PTP; 1.

PROSITE; PSOOGE5; TYR PHOSPHATASE PTP; 1.

PROSITE; PSOOGE5; TYR PHOSPHATASE 2; 1.

PROSITE; PSOOGE 1 TYR PHOSPHATASE 2; 1.

PROSITE; PSOOGE 1 TYR PHOSPHATASE 2; 1.

PROSITE; PSOOGE 1 TYR PHOSPHATASE 2; 1.
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Genew; HGNC:9647; PTPN14.
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                                                                                                                                                                                                    2136 -----IQKPQEXXTDDDEITWG-NDELPIERTWHEDSD-------KD- 2169
                                                                                                                                                                                                                                                                                      2089 KONGKLSEERTEDTDCDG-----SPLPEYFTEATKANGCEEYCEEKVKSESL----- 2135
                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                             63 SDKYELVYPEPLESDTDETVWDVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSKDT 122
                                                                                                                                                                                                                                                          123 ETSVSEKELTQLAQIRPLIFNSSARSAMRDCLNTLQ-----KKEELDIIREFLELEQM 175
                                                                                                                                                                                                                                                                                                                                         TLPDDFNSGNTLQNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEBYFYIATQ 235
                                                                                                                                                                                                                                                                                                                                                                                                                        GPLPETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYMPISL-KEPLEFEHFSVFLET 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLVHCSAGVGRIGVFICVDVVFSAIEKNYSFDIMNIVTQVRKQRCGMIQTKEQYQFCYEI 414
                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Breast carcinoma;

M MEDLINE=95251727; PubMed=7733990;
Smith A.L., Mitchell P.J., Shipley J., Gusterson B.A., Rogers M.V.,
Crompton M.R.,
Crompton M.R.,
I "Pez: a novel human cDNA encoding protein tyrosine phosphatase- and
ezrin-like domains.";
Blochem. Blophys. Rev. Commun. 209:959-965(1995).
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
tyrosine + phosphate.
-!- TISSUE SPECIFICITY: Expressed in a variety of human tissues
including kidney, skeletal muscle, lung and placenta.
-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
                                                                                              6 KVRGKTGRDNDEBBGNSGNLNLRNSLP---SSSQKMTPTKPIFGNKMNSENVKPSHHLSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 FHVTQYPTVRVPQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
MCDI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q15678;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein tyrosine phosphatase, non-receptor type 14 (BC 3.1.3.48)
Protein-tyrosine phosphatase pez).
                                                              26;
                     Length 2485;
              29.1%; Score 653; DB 1; Length 24 34.7%; Pred. No. 5.7e-37; Live 73; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1187 AA.
                                                         149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415 VLEVLONLLA 424
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                 Query Match
Best Local Similarity
Matches 149; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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73

927

239 987

us-09-095-478a-5.rsp

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Pfam, PF00373; Band 41; 1.
Pfam, PF00102; Y phosphatase; 1.
PRINTS; PR00305; BAND41.
PRINTS; PR00700; PRTYPHPHTASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       890 OYKFVCEAILRVYE 903
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Matches 140; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                670
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062130;
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ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license arement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arimura Y., Hinoda Y., Itoh F., Takekawa M., Tsujisaki M., Adachi M., Imai K., Yachi A.; "cDNs cloning of new protein tyrosine phosphatases in the human colon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytoskeleton.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein tyrosine + phosphate.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUMILARITY: Belongs to the protein-tyrosine phosphatase family.
-!- SIMILARITY: Contains 1 PERM domain.
-!- SIMILARITY: Contains 1 PERM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Expression of cytoskeletal-associated protein tyrosine phosphatase PTFH1 mRNA in human heparocellular carcinoma."; J. Gastroenterol. 29:727-732(1994).
-i. FUNCTION: May act at junctions between the membrane and the
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-19196738; PubMed=1648725;
Yang O., Tonks N.K.;

"Isolation of a cDNA clone encoding a human protein-tyrosine
"Isolation of a cDNA clone encoding a human protein-tyrosine
posphatase with homology to the cytoskeletal-associated proteins
band 4.1, ezrin, and talin, ".
Proc. Natl. Acad. Sci. U.S.A. 88:5949-5953(1991).
                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                            01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein tyrosine phosphatase, non-receptor type 3 (BC 3.1.3.48)
Protein-tyrosine phosphatase H1) (Prp-H1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 899-913 FROM N.A.
MEDIJINE=59179278; Pubmed=7874267;
Ikuta S., Itoh F., Hinoda Y., Toyota M., Makiguchi Y., Imai K.
Yachi A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0004725; F:protein tyrosine phosphatase activity; TAS. GO:0006470; P:protein amino acid dephosphorylation; TAS. InterPro; IPR000299; Band 4.1. InterPro; IPR001478; PDZ. InterPro; IPR001478; PDZ. InterPro; IPR001477; PDZ. InterPro; IPR000187; TYR phosphatase. InterPro; IPR000242; TYR_PP.
                                                                                                          913 AA
  1161 MFMIQTIAQYKFVYQVLIQFLQN 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 194-896 FROM N.A.
TISSUE-COlon,
MEDLINE-92327504; PubMed-1626183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fumour Biol. 13:180-186(1992).
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HSSP; P18031; 1PTY.
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MIM; 176877; -.
                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                       HUMAN
                                                                                                                          P26045;
                                                                                 PIN3 HUMAN
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71 PEPLESDIDETVWDVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSKDIETSVSEKE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        564 GRDISEHTHDQV-----VMPIKASRESHSRELALVIRRRAVRSFADFKSEDE 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 LTQLAQIRPLIFNSSARSAMRDCL--NTLQKKBELDIIREFLELELEQM------T 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               714 -YIATQGPLPHTCAQFWQVVWDQKCSLIVWLTTLTERGRTKCHQYWP---DPPDVWNHGG 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        830 SLRVDSEPVLVHCSAGIGRIGVIVIMETAMCLIERNLPIYPLDIVRKÄRDQRAMWVQISS 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 LPDDFNSGNTLQNRDKNRYRDILPYDSTRVPLGKNKDYINASYI------RIVNHBEEY 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 FYIATOGPLPETIEDFWOMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEH-- 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288 PSVFLETPHVTQYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVR 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 RDNDEBEGNSGNINLRNSLPSSSQKWTPTKPIFGNKWNSENVKPS--HHLSFSDKYBLVY
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)
PPDN14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.6%; Score 506; DB 1; Length 913; 32.3%; Pred. No. 2.2e-27; tive 63; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN-TYROSINE PHOSPHATASE.
PHOSPHOCYSTEINE INTERMEDIATE
(BY SIMILARITY).
?? 29A539ACDE2F1515 CRC64;
SMART; SM00295; B41; 1.
SMART; SM00295; B41; 1.
SMART; SM00298; PDZ; 1.
PROSITE; PS00660; FERM_1; 1.
PROSITE; PS00661; FERM_2; 1.
PROSITE; PS00661; FERM_3; 1.
PROSITE; PS00051; FERM_3; 1.
PROSITE; PS00051; PERM_3; 1.
PROSITE; PS00055; TYR_PHOSPHATASE 1; 1.
PROSITE; PS00055; TYR_PHOSPHATASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1189 AA.
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984 TOGPLPHTCHDFWOMVWEQGVNVIAMVTAEEEGGRTKSHRYWP----KLGSKHSSATYG 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1099 QSVRRHTNSVLEGIRTRHPPIVVHCSAGVGRTGVVILSBLMIYCLEHNEKVEVPTMLRFL 1158
                                                                                                                                                                                                                        TQGPLPETIEDFWQMVLENNCNVIAMITRRIECGVIKCYSYWPISLKEPLEFEHFSVFLE 293
808 PSISEPDLTSVKERVKKEPVKERPVSEMPSLEDSIIEREMMIRNLEKQKMTGPQAQKRPL 867
                                                            ---NSSARSAMRDCLNTLQKKEELDIIREFLELEGMTLPDD-- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       343 --VRYVRKSHITG-----PLLVHCSAGVGRTGVFICVDVVFSAIBKNYSFDIMNIVTQM 394
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Lamerdin J.S., McCready P.M., Skowronski E., Viswanathan V.,
Lamerdin J.S., McCready P.M., Dias J., Ramirez M., Stilwagen S.,
Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Garnes J.,
Danganan L., Brler A., Christensen M., Georgescu A., Avila J., Liu S.,
Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,
Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
Arellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,
Olsen A.S., Carrano A.V.;
                                                                                                  868 MLAALINGLSVARVSGREDGRHDATRVPIDERLRALKKKIJEDGAV--FTEYEQ--IPNKKA
                                                                                                                                                                                      181 ---FNSGNTLQNRDKNRYRDILPYDSTRVPL----GKNKDYINASYIRIVNHEBEYFYIA
                                                                                                                                                                                                                                                                                                                                                                                                                                             294 TFHVTQYF-----TVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1039 KFKVITKFRTDSGCYATTGLKVRHLLSGQERTVWHLQYTDWPHHGCPEDVQGFLSYLEEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Feral brain;
MEDLINE-96102179; PubMed-8524829;
Pulido R., Serra-Pagges C., Tang M., Streuli M.;
Pulido R., Serra-Pagges C., Tang M., Streuli M.;
The LAR/FOTP delta/FTP sigma subfamily of transmembrane protein-
tyrosine-phosphatases: multiple human LAR, PTP delta, and PTP sigma
isoforms are expressed in a tissue-specific manner and associate with
the LAR-interacting protein LIP.1.;
Proc. Natl. Acad. Sci. U.S.A. 92:11686-11690(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTNS HUMAN STANDARD, PRT, 1948 AA.

Q1333, Q15718; Q16341;
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Receptor-type protein-tyrosine phosphatase S precursor (EC 3.1.3.48)
(R-PTP-S) (Protein-tyrosine phosphatase sigma) (R-PTP-sigma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-96255038; PubMed-88992885; Bado N., Rutledge S.J., Opas B.E., Vogel R., Rodan G.A., Schmidt A.; "Human protein tyrosine phosphatase-sigma: alternative splicing and inhibition by bisphosphonates."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence analysis of a 2.5 Mb region in 19p13.3.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          395 RKORCGMIQTKBOYOFCYEIVLEVLON 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bone Miner. Res. 11:535-543(1996).
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MEDLINE=92119637; Pubmed=1370651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
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                                                            141 IF-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its who non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               636 GGGGTVNKRHSLEVMNSMVRGMEAMTLKSLNIPMARRNTLREQGPSEETGGHEVHG---L 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPEYPGPRKSVS---NGALRODOGTPLPAMARCRVLRHGPSKALSVSRAEQLAVNGASIG 807
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                                                                                                                                                                                                                                                                              DEVELOPMENT
                                                                                                        MEDLINE=94354845; PubMed=8074693;
Sawada M., Ogata M., Fujino Y., Hamaoka T.;
Savada M., Ogata M., Fujino Y., Hamaoka T.;
Cobrox cloning of a novel protein tyrosine phosphatase with homology
to cytoskeletal protein 4.1 and its expression in T-lineage cells.";
Biochem. Biophys. Res. Commun. 203:479-484(1994).
-!- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF T CELL DEVELOPMENT
-!- CATALITIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                        tyrosine + phosphate.

TISSUE SPECIFICITY: Thymus; in cells of both hematopoietic and non-hematopoietic origins.
SIMILARITY: Contains 1 FERM Gomain.
SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153, Indels 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1189;
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PHOSPHOCYSTEINE INTERMEDIATE
(BY SIMILARITY).
POLY-PRO.
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1189 AA; 135030 MW; 2BB5B5F9C723303 CRC64;
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MGD; MGI:102467; Ptpn14.

MGD; MGI:102467; Ptpn14.

InterPro; IPR000249; Band 4.1.

InterPro; IPR000249; TYR_phosphatase.

InterPro; IPR000249; TYR_phosphatase.

Pfam; PF00102; Y_phosphatase; I.Promoro; PR00102; Y_phosphatase; I.Promoro; PRTYPHPHTASE.

PRINTS; PR00035; BAND41.

PRINTS; RM00194; PTPC; I.SMART; SM010194; PTPC; I.SMART; PROSTITE; PS000561; PTRM_2; I.SMART; PROSTITE; PS000383; TYR_PHOSPHATASE_1; I.SMARTINGTITE; PS00056; TYR_PHOSPHATASE_2; I.SMARTINGTITE; PS00056; TYR_PROSPHATASE_2; I.SMARTINGTITE; PS0000
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27.0%; Pred. No. 8e-27;
tive 79; Mismatches 1
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153; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor protein tyrosine pho. . .; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              placenta and liver.
SIMILARITY: BELONGS TO THE RECEPTOR CLASS OF THE PROTEIN-TYROSINE
PHOSPHATASE FAMILY.
Adachi M., Sekiya M., Arimura Y., Takekawa M., Itoh P., Hinoda Y., Imai K., Yachi A.;
"Protein-tyrosine phosphatase expression in pre-B cell NALM-6.";
"Protein-Tes. 52:737-740(1992).
-! - FUNCTION: Interacts with LAR-interacting protein LIP.1.
-! - CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
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SMART; SMOLLS, 2.
SMART; MO194; PTPC, 2.
SMART; MO194; PTPC, 2.
SMART; MO194; PTPC, 2.
PROSITE; PS50855; TYR_PHOSPHARASE_1; 2.
PROSITE; PS50055; TYR_PHOSPHARASE_2; 2.
Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
TYPE PROSITE; PS50055; TYR_POSPHARASE PTP; 2.
Hydrolase; Receptor; Glycoprotein; Milernative splicing; Repeat.

"Analysis of the property of the 
                                                                                                                                                                                                                                                                                         Isoid=013332-2; Sequence=VSP_050021;
Name=PTPS-MEB;
Isoid=013332-3; Sequence=VSP_050022, VSP_050026, VSP_050027;
                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q13332-5; Sequence=VSP 050023, VSP 050025; TISSUE SPECIFICITY: DEtected in all tissues tested except for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domain.
-!- SIMILARITY: Contains 8 fibronectin type III domains.
-!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
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CYTOPLASMIC (POTENTIAL)
                                                                                                                     tyrosine + phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
Comment=Alternative splicing; Named isoforms=5;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                            IsoId=013332-4; Sequence=VSP_050024;
                                                                                                                                                                                                                                                    IsoId=Q13332-1; Sequence=Displayed;
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InterPro; IPR003961; FN III-like.
InterPro; IPR003961; FN III-like.
InterPro; IPR003101; FN III-like.
InterPro; IPR00110; Ig-like.
InterPro; IPR000389; Ig-C2.
InterPro; IPR000389; Ig-C2.
InterPro; IPR000389; Ig-C2.
InterPro; IPR000424; TYR phosphatase.
Pfam; PF00041; fn3; 8.
Pfam; PF00104; In3; 8.
Pfam; PF00105; Tybophatase; 2.
Pfam; PF00105; Tybophatase; 2.
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GO; GO:0005887; C:integral to plasma
GO; GO:0005001; F:transmembrane recep
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PRINTS; PRODO0; PRIYPHPHTASB.
SWART; SMO060; FNJ; 7.
SWART; SMO0408; IGG22, 3.
SWART; SMO0194; PTPC; 2.
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                                                                                                                                                                                                                                                                          Name=PTPS-MEA;
                                                                                                                                                                                                                                                                                                                                                          Name=PTPS-MEC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 LELEGATLPDD-----FNSGNTLQNRDKNRYRDILPYDSTRVPLG-----KNKDYINAS
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S - G (in isoform PTPS-MEB).

/FIGEWORP 050026.

T - HP (IN REF. 2).

SA -> RP (IN REF. 2).

GAGGGCPR -> REPA (IN REF. 2).

GAGGGCPR -> REPA (IN REF. 2).

GAGGGCPR -> REPA (IN REF. 2).

T -> P (IN REF. 2).

T -> S (IN REF. 2).

T -> S (IN REF. 2).

F -> S (IN REF. 2).

T -> S (IN REF. 2).

W -> S (IN REF. 2).

W -> S (IN REF. 4).

W -> A (IN REF. 4).
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(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                    PHOSPHOCYSTEINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                                                                     PHOSPHOCYSTEINE INTERMEDIATE (BY
                                                  FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 8.
FROTEIN-TYROSINE PHOSPHATASE 1.
FROTEIN-TYROSINE PHOSPHATASE 2.
                                                                                                                                                                                                                    44
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PTIG=VSP 050023.
Hissing (In isoform PTPS-MEC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FTIG=VSP 050024.
7 -> I (in isoform PTPS-F4-7).
FTIG=VSP 050025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isoform PTPS-MEA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Missing (In isoform PTPS-MEB)
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N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
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/FTId=VSP 05
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1587 V ->
1705 N ->
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CARBOHYD
                      EMBL;
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    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22064388; PubMed=12089527;
Ruivenkamp C.A.L., van Wezel T., Zanon C., Stassen A.P.M., Vlcek C.,
Csikos T., Klous A.M., Tripodis N., Perrakis A., Boerrigter L.,
Groot P.C., Lindeman J., Mooi W.J., Meijjer G.A., Scholten G.,
Dauwerse H., Paces V., van Zandwijk N., van Ommen G.J.B., Demant P.;
"Ptprj is a candidate for the mouse colon-cancer susceptibility locus
"Col and is frequently deleted in human cancers.";
Nat. Genet. 31:295-300(2002).
--- FUNCTION: May contribute to the mechanism of contact inhibition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tyrosine + phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
PITH: N- and O-glycosylated.
DISEASE: Defects in PTPRJ are found in cancers of colon, lung, and breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95086212; PubMed=7994032;
Honda H., Inazawa J., Nishida J., Yazaki Y., Hirai H.;
"Molecular cloning, characterization, and chromosomal localization of
a novel protein-tyrosine phosphatase, HPTP eta.";
Blood 84:4186-4194(1994).
                                                                                                                             PITO THURAN SIANDALI, FRI; 1337 A4.

O12913: O15255; O8NHMA;
O1-NOV-1997 (Rel. 35, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
Protein-tyrosine phosphatase eta precursor (EC 3.1.3.48) (R-PTP-eta)
(HPTP eta) (Protein-tyrosine phosphatase receptor type J) (Density enhanced phosphatase-1) (CD148 antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell growth.
CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
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                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95024024; PubMed=7937872; Oestman A., Yang O., Tonks N.K.; Texpression of DEP-1, a receptor-like protein-tyrosine-phosphatase, is enhanced with increasing cell density."; Proc. Natl. Acad. Sci. U.S.A. 91:9680-9684(1994).
                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Contains 1 protein-tyrosine phosphatase domain. SMILARITY: Contains 5 fibronectin type III domains. DATABASE: NAME-BROW, NOTE-CD guide CD148 entry, WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd148.htm".
                                                                                                                     PRT; 1337 AA
EMBL, D37781, BAA07035.1; -.
EMBL, AF387844, AAM69432.1; -.
EMBL, AF387823, AAM69432.1; JOINED.
EMBL, AF387824, AAM69432.1; JOINED.
EMBL, AF387825; AAM69432.1; JOINED.
EMBL, AF387826; AAM69432.1; JOINED.
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MIM; 600925; ...

R GO; GO:000501; P:transmembrane receptor protein tyrosine pho. ..;

GO; GO:0005001; P:transmembrane receptor protein tyrosine pho. ..;

GO; GO:0005001; P:transmembrane receptor protein tyrosine pho. ..;

GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.

GO; GO:000169; P:transmembrane receptor protein tyrosine kin. ..;

R InterPro; IPR003961; FN_III.like.

InterPro; IPR003961; FN_III.like.

R InterPro; IPR003961; FN_III.like.

R InterPro; IPR003961; FN_III.like.

R InterPro; IPR003961; FN_III.like.

R Pfam; Pr001010; Y Phosphatase.

R PRART; SM0060; FN3; 8.

R SMART; SM0060; FN3; 8.

R SMART; SM00989; FN3; 8.

R PROSITE; PS00383; TYR PHOSPHATASE 1; 1.

R PROSITE; PS00383; TYR PHOSPHATASE 2; 1.

R PROSITE; PS00585; TYR PHOSPHATASE 2; 1.
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FIBRONECTIN TYPE-111 1.
FIBRONECTIN TYPE-111 3.
FIBRONECTIN TYPE-111 4.
FIBRONECTIN TYPE-111 4.
FROMETHY TYPE-111 5.
PROTEIN-TYPE-111 5.
PHOSPHOCYSTEINE PHOSPHAASE.
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                                                      EMEL; AF387830; AAM69432.1; JOINED. EMEL; AF387831; AAM69432.1; JOINED. EMEL; AF387831; AAM69432.1; JOINED. EMEL; AF387833; AAM69432.1; JOINED. EMEL; AF387834; AAM69432.1; JOINED. EMEL; AF387845; AAM69432.1; JOINED. EMEL; AF387855; AAM69432.1; JOINED. EMEL; AF387891; AAM69432.1; JOINED. EMEL; AF387891; AAM69432.1; JOINED. EMEL; AF387841; AAM69432.1; JOINED. EMEL; AF387841; AAM69432.1; JOINED. EMEL; AF387842; AAM69432.1; JOINED. EMEL; AF38782; AF783; PTPRJ.
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RT "Identification of a novel RT homology to the cytoskelet RL FEBS Lett. 356:351-356 (195 C -1 CATALYTIC ACTIVITY: PF C LYCOSINE + phosphate. CC -1 ALTERNATIVE PRODUCTS: CC Name=1; CC Name=1; CC ISOId=062728-1; Sequect CC -1 TISSUB SPECIFICITY: Pe CC -1 SIMILARITY: Delongs CC C-1 SIMILARITY: Delongs CC C-1 SIMILARITY: Delongs CC CC -1 SIMILARITY: Belongs CC CC -1 SIMILARITY: CC -1 SIMIL	CC This SWISS-PROT entry is c CC between the Swiss Institut CC the Buropean Bioinformatic CC use by non-profit insti CC modified and this statement CC entities requires a licens	DR EMBL; U17971; AAA62153.1; DR EMBL; U18293; AAA62154.1; DR PIR; S51005; S51005. DR HASP, Q06124; 2SHP. DR INTERPO; IPR000299; Band DR INTERPO; IPR000387; TYR. DR INTERPO; IPR000242; TYR.		DR PROSITE; PS:003.7; FEMM.3; DR PROSITE; PS:0038; TYR_PHOS DR PROSITE; PS:0055; TYR_PHOS DR PROSITE; PS:0055; TYR_PHOS FY DOMAIN 922 1175 FT ACT_SITE 1109 1109	VARSPLIC 1 83 SEQUENCE 1175 AA;	Query Match Best Local Similarity 28.2% Matches 146; Conservative Qy 44 IFGNONSENVEP Db 677 VFSDKVKQEGTEEQGSC Qy 98 DSETAGPS Db 730 PRITAAFSQEQUAVE	Oy 125SVSEKELTQLA Db 790 HGLLTPSMSESDLTTS OY 159 -KKEELDIIR Db 840 MKKTRADAKKIGPLKLA OY 188
T CARBOHYD 582 582 N-LINKED (GLCNAC) (POTENTIAL). T CARBOHYD 603 603 N-LINKED (GLCNAC) (POTENTIAL). T CARBOHYD 618 628 N-LINKED (GLCNAC) (POTENTIAL). T CARBOHYD 628 628 N-LINKED (GLCNAC) (POTENTIAL). T CARBOHYD 637 666 666 N-LINKED (GLCNAC) (POTENTIAL). T CARBOHYD 669 666 N-LINKED (GLCNAC) (POTENTIAL). T CARBOHYD 701 701 N-LINKED (GLCNAC) (POTENTIAL). T CARBOHYD 701 702 N-LINKED (GLCNAC) (POTENTIAL). T CARBOHYD 701 701 N-LINKED (GLCNAC) (POTENTIAL). T CARBOHYD 700 700 N-LINKED (GLCNAC) (POTENTIAL). T CARBOHYD 701 N-LINKED (GLCNAC) (POTENTIAL). T CARBOHYD 910 N-LINKED (GLCNAC) (POTENTIAL).	T / FTIG=10APR 015905. T VARIANT 276 276 Q -> P (in colon cancer; somatic mutation). T / FTIG=VAR 015906. T CONFLICT 261 261 G -> D (IN REF. 1). T CONFLICT 918 929 YNGKLEPLGSYR -> LQWEAGTSGLLP (IN REF. 2). Q SEQUENCE 1337 AA; 145926 WW, R6752D521C4B6AFE CRC64;	Query Match 21.7%; Score 487; DB 1; Length 1337; Best Local Similarity 34.9%; Pred. No. 7.4e-26; Matches 110; Conservative 63; Mismatches 114; Indels 28; Gaps 8; Matches 110; Conservative 63; Mismatches 114; Indels 28; Gaps 8; y 119 SKDTBTSVSEKELTQLAQIRPLIFNSSARSAMRDCLNTLQKKEELDIRREFLELEQ 174 ;	y 175 MTLPDDFNSGNTLQNRDKORRYRDILPYDSTRVPLGKUKDYINASYIRIVNHBEEYF 230 ::::::::::::::::::::::::::::::::::::	y 291 FLETFHVTQYFTVRVPQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVR-YV 346	y 407 QYQFCYBIVLEVLQN 421	ESULT 7 TINL RAT D _FINL RAT C 062728; 062732; T 01-NOV-1997 (Rel. 35, Created) T 01-NOV-1997 (Rel. 35, Last sequence update) T 01-CCT-2003 (Rel. 42, Last annotation update) E Protein tyrosine phosphatase, non-receptor type 21 (BC 3.1.3.48) R Protein tyrosine phosphatase 2B).	Status norvegicus (Rat). C Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; C Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. X NCBI_TaxID=10116; N [1] N [1] SEQUENCE FROM N.A. (ISOFORMS 1 AND 2E). C STRAIN=Sprague-Dawley; X MEDLINE=59104446; PubMed=7805871; X MEDLINE=59104446; PubMed=7805871; A L'Abbe D., Barville D., Tong Y., Stocco R., Masson S., Ma S., A Fantus G., Shen S.H.;

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PCASVTPVTGPLHIFEPKSHVTEPEKRAKDISPVHLVMETHQPRR 789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAQIRPLIFNSSARSAMRDCL------NTLO----- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --- 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---SHHLSFSDKYBLVYPEPLESDTDETVWDVSDRSLRNRWNSM 97
el protein tyrosine phosphatase with sequence
etal proteins of the band 4.1 family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6%; Score 484.5; DB 1; Length 1175;
2%; Pred. No. 9.3e-26;
69; Mismatches 141; Indels 161; Gaps
                                                                   Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                        guence=VSP 000498;
ParticularIy abundantly in adrenal glands.
; I FERM domain.
to the protein-tyrosine phosphatase family.
ubfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---BFLELEQMTLEDDFNSGNTL------
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OSPHATASE PTP; 1.
OSPHATASE 2; 1.
8keleton; Hydrolase; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN-TYROSINE PHOSPHATASE.
PHOSPHOCYSTEINE INTERMEDIATE
(BY SIMILARITY).
Missing (in isoform 2B).
/PTIG=VSP 000498.
| PTIG=VSP 000498.
                                                                                                                                         licing; Named isoforms=2;
                                                                                                                                                                                          quence=Displayed;
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Iphosphatase.
IPP.
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modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb.sib.ch).
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1912 AA; 214759 MW;
                                                           EMBL; L38929; AAC41749.1; -. EMBL; X54133; CAA38068.1; -. PIR; A56178, A56178, A56178; PASSP; PLOG52; 1 YFO. Genew; HGNC:9668; PTPRD.
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832
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SEQUENCE
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the EWBL outstation-the European Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                     960 SVSGIEWDYIAIQGELQNICQDFWQMVWEQGVAIIAMVIAEEBGGREKSFRYWP----R 1014
                                                                                                                                900 EYERILKKRLVDGECSTARLPENARRNRPQDVLPYDDARVELVPTKENNTGYINASHIKV 959
                                                                                                          283 LEFEHFSVFLETFHVTQYF-----TVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPAS 335
                                               223 VNHEEBYFYIATOGPLPETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEP 282
                                                                                                                                                                        336 ADFFIKYVRYV----RKSHITG-----PLLVHCSAGVGRTGVFICVDVVFSAIEKNYS 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pulido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M., "Molecular characterization of the human transmembrane protein-
tyrosine phosphatase delta. Byidence for tissue-specific expression alternative human transmembrane protein-tyrosine phosphatase delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Placents;
MEDLINE-91006018; PubMed=2170109;
MEDLINE-91006018; PubMed=2170109;
MEDLINE-91006018; PubMed=2170109;

"Strueger N.X., Streuli M., Saito H.,
"Structural diversity and evolution of human receptor-like protein tyrosine phosphateases.",
EMBO J. 9:1241-1252(1990).
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=2; Synonyms=Kadney;
IsoId=P23468-2; Sequence=VSP_005147, VSP_005148, VSP_005149;
Name=3; Synonyms=Retal Drain;
IsoId=P23468-3; Sequence=VSP 005150;
PTM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOWAIN FROM THE TRANSMEMBRANE SEGMEN.
SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 8 fibronectin type III domains.
SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1991 (Rel. 20, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
delta protein-tyrosine phosphatase delta precursor (EC 3.1.3.48) (R-PTP-PTP-PTR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                         385 FDIMNIVTOMRKORCGMIQTKEQYQFCYBIVLEVLQN 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tyrosine + phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bvent=Alternative splicing, Named isoforms=3;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-1178.
                                                                                                                                                                                                                                                                                                                                                     PRT; 1912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P23468-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. Chem. 270:6722-6728(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95204468; PubMed=7896816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 390-1912 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                   HUMAN
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NAMAN
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(See http://www.isb-sib.ch/announce/
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R->A: 2.5-FOLD REDUCTION IN CLEAVAGE
W; 3AE8CBCD32182E26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
Missing (in isoform 2).
/FIId=VSP 005147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN-TYROSINE PHOSPHATASE DELTA.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIBRONECTIN TYPE III 1.
PIBRONECTIN TYPE III 1.
PIBRONECTIN TYPE III 3.
PIBRONECTIN TYPE III 4.
PIBRONECTIN TYPE III 6.
PIBRONECTIN TYPE III 6.
PIBRONECTIN TYPE III 6.
PIBRONECTIN TYPE III 7.
PROFEIN-TYROSINE PHOSPHATASE 1.
PROTEIN-TYROSINE PHOSPHATASE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHOCYSTRINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (in isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=VSP_005148.
Missing (in isoform 2)
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N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
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168
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                                                                                                                                                                                             170 LELEQMILPDD-----FNSGNILQNRDKNRYRDILPYDSTRVPLG-----KNKDYINAS 218
                                                                                                                                                                   219 YIRIVNHEEBYFYIATQGPLPETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPIS 278
                                                                                                                                                                                                                                                   279 LKEPLEFBHFSVF-LETFHVTQYPTVRVFQIVKKSTGKSQCVXHLQPTKWPDHGTPASAD 337
                                                                                                                                                                                                                                                                                                                                  FFIKYVRYVRKSH----ITGPLLVHCSAGVGRTGVFICVDVVFSAIBKNYSFDIMNIVTQ 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Higashitanii H., Arii S., Buntani M., Imamura M., Kaneko Y., Takenawa J., Nakayama H., Fujita J.; Takenawa J., Nakayama H., Fujita J.; Takenawa J., Nakayama H., Fujita J.; Endanced expression of multiple protein tyrosine phosphatases in the regenerating mouse lives: isolation of PTP-RL10, a novel cytoplasmictype phosphatase with sequence homology to cytoskeletal protein
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oncogene 10:407-414(1995).
-!- FUNCTION: May be involved in the regulation of growth and differentiation of liver cells.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine + phosphate.
-!- TISSUB SPECIFICITY: Liver.
-!- SIMILARITY: Contains 1 FERM domain.
-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last amotation update)
Protein tyrosine phosphatase, non-receptor type 21 (EC 3.1.3.48)
(Protein-tyrosine phosphatase PTP-RIIO).
                                           21;
        DB 1; Length 1912;
    21.5%; Score 481.5; DB 1; Length 40.2%; Pred. No. 2.8e-25; ive 45; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1176 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1879 LRTORPAMVOTEDOVOFSYRAALEYL 1904
                                                                                                                                                                                                                                                                                                                                                                                                                394 MRKORCGMIQTKEQYOFCYEIVLEVL 419
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InterPro; IPR000387; TYR phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Liver;
MEDLINE=95140431; PubMed=7838537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D37801; BAA07053.1; -. PIR; IS8345; IS8345.
Query Match
Best Local Similarity 40.2
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; 158345; 158345.
HSSP; P29350; 1GWZ.
MGD; MGI:1344406; Ptpn21.
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Q62136;
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299 QYF-----TVRVPQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVR---- 347
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857 AALNGLSLSRIPIPDEGKEVSTRATNDERCKVLEQRLEQGMVFTEYERILKKRLVDGECS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 PETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLBTFHVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1032 TRFRIDSGCYATTGLKMKHILTGGERTVWHILQYTDWPEHGCPEDLKGFLSYLBEIQSVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          348 -----KSHITGPLLVHCSAGVGRTGVPICVDVVPSAIBKNYSFDIMNIVTQMRKQRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 -----ONRDKNRYRDILPYDSTRVPLGKNKD----YINASYIRIVNHBBBYFYIATQGPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVSEKELTQLAQI------RPLIFNSSARSAMRDCLNTL--QKKGBLDIIR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PESULT 10
PIN4 HUMAN STANDARD; PRT; 926 AA.

AC P29074;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 42, Last annotation update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 4 (EC 3.113.48)
DE Protein-tyrosine phosphatase MEG1) (PrPase-MEG1) (MEG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 481; DB 1; Length 1176;
Pred. No. 1.6e-25;
74; Mismatches 155; Indels 130;
                                                                                                                                                                                                                                                                                                                                                                                                                     3 PHOSPHATASE
INTERMEDIATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            565 572 POLY-PRO.
1176 AA; 133490 MW; 529FBE22F1335B75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---EPLELEQMILPDDPNSGNTL-------
                                                                                                                                                                                         PROSITE; PSOGGG; FERM_1; 1.
PROSITE; PSOGGG; FERM_2; 1.
PROSITE; PSOGGG; FERM_3; 1.
PROSITE; PSOGOS; TYR PHOSPHATASE 1; 1.
PROSITE; PSGOGS; TYR PHOSPHATASE PTP; 1.
PROSITE; PSGOGS; TYR PHOSPHATASE PTP; 1.
PROSITE; PSGOGS; TYR PHOSPHATASE 2; 1.
PROSITE; PSGOGS; TYR PROSITE 1.
PROSITE 3.08
PROFILE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN-TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHOCYSTEINE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1151 MLVQTLGQYTFVYRVLIQFLKS 1172
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InterPro; IPR000242; Tyr_PP.
Pfam; PP000373; Band 41; 1.
Pfam; PP00102; Y_phosphata8e; 1.
PRINTS; PR00305; BAND41.
PRINTS; PR00700; PRTYPHPHTASE.
SMART; SM00295; B41; 1.
SMART; SM00194; PTPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.5%;
28.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343
                                                                                                                                                                                                                                                                                                                                                                                                                                                1110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   1110
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Matches 127; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                 29
517
677
852
SM00194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        819
                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           549
                                                                                                                                                                                                                                                                     ACT_SITE
                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                       DOMAIN
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STITITES
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EMBL; BC010674; AAH10674.1; -
EMBL; BC010674; AAH10674.1; -
HSSP; P29350; J44105.
HSSP; P29350; J44105.
MIN; J16878; -
Genew; HGNC:9656; PTPN4.
MIN; J16878; -
GO; GO:0005737; C:Cytoplasm; TAS.
GO; GO:0005737; C:Cytoplasm; TAS.
GO; GO:0004726; F:non-membrane spanning protein tyrosine phos. .; TAS.
GO; GO:0004726; F:non-membrane spanning protein tyrosine phos. .; TAS.
GO; GO:0004726; F:non-membrane spanning protein tyrosine phos. .; TAS.
InterPro; IPR000299; Bazd 4.1.
InterPro; IPR000299; TYP_PP.
Pfam; PP00313; Band 41; T.
Pfam; PP00313; Band 41; T.
Pfam; PP00315; PR00915; Pposphatase; 1.
Pfam; PP00315; BAND41.
PRINTS; PR00935; BAND41.
PRINTS; PR00935; BAND41.
SMART; SM00228; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                             MEDLINE=22888257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Nagmer L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buttow K.H., Schemen C.M., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchench L., Marusina R., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Donaldo M.F., Casavant T.L., Scheetz T.E.,
Stapleton M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,
Brownstein M.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergen E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevohenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Gchen E.D., Dickson M.C.,
Schnerch A., Schein J.E., Jones S.J.M., Marra R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                             MEDLINE-91288564; PubMed-1648233;
Gu M., York J.D., Warshawsky I., Majerus P.W.;
"Identification, cloning, and expression of a cytosolic megakaryocyte
protein-tyrosine-phosphatase with sequence homology to cytoskeletal
protein 4.1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tyrosine + phosphate.
-!- SIMILARITY: Contains 1 FERM domain.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 88:5867-5871(1991).
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                     SEQUENCE FROM N.A.
                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytoskeleton
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84 DVSDRSLRNRWNSMDSBTAGPSKTVSPVLSGSSRLSKDTBTSVSBKELTQLAQIRPLIFN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          648 EGLITGTVLTQFDQLYRKKPGMTMSCAKLPQNISKNRYRDISPYDATRVILKGNEDYINA 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----QMTLP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYIR-----IVNHEBERYFYIATQGPLPETIEDFWQMVLENNCNVIAMITREIECGVIK 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQ---IVKKSTGKSQCVKHLQFTKW 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDHGTPASADFFIKYVRYVRKSHI---TGPLLVHCSAGVGRTGVFICVDVVFSAIEKNYSF 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 NIALIRNSLPSSSOKMTPTKPIFGNKMNSENVKPSHHLSFSDKYELVYPBPLBSDTDETVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDFNSGNTL-------QNRDKNRYRDILPYDSTRVPLGKNKDYINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHOYWP----BPTGSSSYGCYOVTCHSBEGNTAYIFRXMTLFNQEKNESRPLTQIQYLAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CS7BL/6J;
MEDLINE=22730707; PubMed=11423001;
MEDLINE=22730707; PubMed=11423001;
Besco J.A., Frostholm A., Popesco M.C., Burghes A.H.M., Rotter A.,;
"Genomic organization and alternative splicing of the human and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTPT MOUSE STANDARD; PRT; 1454 AA.
Q99M80; Q99M81; Q99M82; Q9JIZ1; Q9JIZ2; Q9JKC2; Q9JLP0;
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Receptor-type protein-tyrosine phosphatase T precursor (EC 3.1.3.48)
(R-PTP-T) (RPTP-rho) (MRPTPFHD) (RPTPmam4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUTENCE FROM N.A. (ISOFORMS 2 AND 5), AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 27.9%; Pred. No. 1.8e-25; 7; Conservative 67; Mismatches 172; Indels 89
                                                                                                                                                                                                                                                                                                                                                        PHOSPHOCYSTEINE INTERMEDIATE
                                                                                                                                                                                                                                                                                                                          PROTEIN-TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY).
926 AA; 105911 MW; 4DACGA87A675CFB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 SSARSAMRDCLNTLOKKEELDIIREFLELB--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        386 DIMNIVIQMEKQRCGMIQTKEQYQFCYBIVLEVLQ 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00660; FERM 1; 1.
PROSITE; PS00661; FERM 2; 1.
PROSITE; PS01061; FERM 3; 1.
PROSITE; PS01006; PDZ, 1.
PROSITE; PS01006; PDZ, 1.
PROSITE; PS01066; TYR PHOSPHATASE 1; 1.
PROSITE; PS00566; TYR PHOSPHATASE 2; 1.
PROSITE; PS00565; TYR PHOSPHATASE PTP; 1.
Structural protein; Cytoskeleton; Hydrolase.
DOMAIN 29 312 PERM.
```

RPTPrho genes.";
BMC Genomics 2:1-1(2001).

RPTPrho

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insula SPECIFICITY: Expression is restricted to the CNS.

1 ISSUE SPECIFICITY: Expression is restricted to the CNS.

Distributed throughout the brain and spinal cond.

1 DEVELOPMENTAL STAGE: Exceptionally high levels found in the cortex and olfactory bulbs during perinatal development and are downregulated during postnatal week 2. Expression in the cereballar cortex is restricted to the granule cell layer of lobules 1-6.

Anterior and posterior compartments become discernible only during postnatal weeks 2 and 6.

1 SIMIARITY: Contains 1 MAM domain.

2 SIMIARITY: Contains 2 immunoglobulin-like C2-type domain.

3 SIMIARITY: Contains 4 fibronectin type III domains.

3 INIARITY: Contains 2 protein-tyrosine phosphatase domains.
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).
Mizuta M., Bergman B., Miki T., Hutton J.C.;
"Molecular cloning and functional characterization on mouse receptor-like protein tyrosine phosphatase, mRPTPrho, which mediates cell-cell addhesion of pancreatic beta cells.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                      Besco J.A., Frostholm A., Popesco M.C., Burghes A.H.M., Rotter A., BMC Genomics 2:5-5(2001).
                                                                                                                                                    [3] SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
Buchli A.D., Zimmermann D.R., Pfister P., Vaughan L.;
"RPTPmam4: a fourth member of the MAM family of receptor protein tyrosine phosphatases expressed in adult brain.";
tyrosine phosphatases expressed in adult brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=3; Synonyms=RPTPrho2;
IsoId=Q99M80-3; Sequence=VSP_007803, VSP_007804;
Name=4; Synonyms=RPTPrho1;
IsoId=Q99M80-4; Sequence=VSP_007803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=099M80-2; Sequence=VSP_007803, VSP_007806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tyrosine + phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=5;
Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=099M80-1; Sequence=Displayed;
                                                                                      MEDLINE=22730717; PubMed=11814386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF152556; AAD34158.4; -. EMBL; AY026861; AAK18741.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AY026862; AAK18742.1; -. AY026863; AAK18743.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=2;
                                                                  ERRATUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
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R -> RHPAEHTVGTATLGRAASPGM (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FIId=VSP 007804.
R -> RRNAYSYSYILSOR (in isoform 5).
/FIId=VSP 007805.
                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                 FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
PROTEIN-TYROSINE PHOSPHATASE 1.
PROTEIN-TYROSINE PHOSPHATASE 2.
PHOSPHOCYSTEINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Tid=VSP 007803.
-> RRNAYSYSYYL (in isoform 3).
                                                                                                                                                                                                                                                                                                                                                          PHOSPHOCYSTEINE INTERMEDIATE (BY
                                                                                                                                                                                                                                   RECEPTOR-TYPE PROTEIN-TYROSINE PHOSPHATASS T. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISSING (IN REF. 1).
R -> P (IN REF. 1).
GGCS -> RGYP (IN REF. 1).
A -> T (IN REF. 4; AAF82401).
I -> V (IN REF. 4; AAF82401).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 and isoform 5)
                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Missing (in isoform 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  007803
                                                                                                                                                                                                                                                                                    IG-LIKE C2-TYPE
                   HSSP; P28827; IRPM.

MGD; MGI:1321152; Ptprt.

InterPro; IPR0003961; FW III.

InterPro; IPR000398; MAM domain.

InterPro; IPR0003595; PTPC motif.

InterPro; IPR0003595; PTPC motif.

InterPro; IPR0003595; PTPC motif.

InterPro; IPR0003595; PTPC motif.

Pfam; PF00041; fn3; 3.

Pfam; PF00041; fn3; 3.

Pfam; PF00102; Y_Dhosphatase; 2.

PRINTS; PR00020; MAMDOMAIN.

PRINTS; PR00020; MAMDOMAIN.
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AF244125; AAF44712.1; -. AF162856; AAF82400.2; -. AF162857; AAF82401.1; -.
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1095 VHCSAGAGRIGCFIAIDTWLDWAENEGVVDIFNCVRELRAQRVNLVQTERQYVFVHDAIL 1154
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                                                                                                                                                                                                                                                                                                                  813
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                                                                                                                                                                                                                                                                                                                                                                                                           | : | | : | | | 874 PRDQFQPAL-----RVADLLQHITQMKRGQGYGFKEEYEALPEGGTASWDTAKED--- 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          977
                                                                                                                                                                                                                                                                                                                                                                    814 VASTDKPTAKLGTNRNDEGFSSSSQDVNGFTDGSRGELSQPTLTIQTHPYRTCDPVEMSY 873
                                                                                                                                                                                                                                                                                                                                                                                             ---QIRPLIFNSSARSAMRDCLNTLQK-----KEBLDIIREFLELEQMTLPDDFNS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                               GNTLQNRDKNRYRDILPYDSTRVPL----GKNKDYINASYIRIVNHBBEYFYIATQGPE 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVT 298
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                                                                                                                                                                                                                                    15 NDEEEGNSGNIALARNSLPSSSOKMTPTKPI ---- FGNKMNSENVKPSHHLSFSDKYELVY
                                                                                                                                                                                                                                                 761 ----EKQVDNTVKMAGVIAGLLMFIIILLGVMLTIKRRKLAKKQKETQS---GAQREMGP
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10-OCT-2003 [Rel. 42, Last sequence update)
10-OCT-2003 [Rel. 42, Last annotation update)
Receptor-type protein-tyrosine phosphatase T precursor (BC 3.1.3.48)
(R-PTP-T) [RPTP-Th0].
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                                                                                                                                                                                21.3%; Score 477.5; DB 1; Length 1454; 28.5%; Pred. No. 3.7e-25; tive 65; Mismatches 160; Indels 119;
                           ; AAF82401).
                                                                             AAF82401).
AAF82401).
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                               66 L -> I (IN REF. 4; AAFB2401)
69 T -> S (IN REF. 4; AAFB2401)
163012 MW; C60464F7B423F8A8 CRC64;
                                                     AAF82401)
                                                                                                                    4; AAFB2401)
                 AAF82401)
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T -> S (IN REF. 4; A)

G -> T (IN REF. 4; A)

TD -> N (IN REF. 4; A)

D -> A (IN REF. 4; A)

H -> H (IN REF. 1).

H -> H (IN REF. 1).

H -> H (IN REF. 1).

H -> V (IN REF. 1; A)

E -> V (IN REF. 1; A)

E -> V (IN REF. 1; A)

E -> V (IN REF. 1; A)

T -> S (IN REF. 1; A)

T -> S (IN REF. 1; A)
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1266 126
1269 126
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Best Local Similarity
Matches 137; Conserv
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SEQUENCE FROM N.A.

MEDLINE=21638749; PubMed=11780052;

MEDLINE=21638749; PubMed=11780052;

MEDLINE=21638749; PubMed=11780052;

Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,

Denoukas P., Matthews L.H., Ashurst J., Babage A.K., Bagguley C.L.,

Basley J., Barlow K.F., Blakey S.E., Eridgeman A.M., Brown A.J.,

Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,

Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

Clegg S., Cobley V.B., Collier R.E., Connor R.E., Corby N. R.,

Coulson A., Coville G.J., Dedman R., Dhami P.D., Dunn M.,

Blington A.G., Frankland J.A., Fraser A., French L., Garner P.,

Raffington A.G., Frankland J.L., Fraser A., Prench L., Garner P.,

Blington A.G., Frankland J.L., Heath P.D., How. J., Howden P.J.,

Huckle E., Hunt A.R., Hunt S.E., Vekosch K., Johnson D.,

RAY M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

Lehvaeslaho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,

Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,

Anines S.A., Mistry D., Moore M.J.F., Mullikan J.C., Nickerson T.,

Anines S.A., Mistry D., Moore M.J.F., Mullikan J.C., Nickerson T.,

Anines S.A., Mistry D., Moore M.J.F., Mullikan J.C., Nickerson T.,

Phillimore B.J.C.T., Prachalingam S.R., Plumb R.W., Ramsay H.,

Rice C.M., Ross M.T., Socott C.E., Sehra H.K., Shownkeen R., Sims S.,

Marsh R.M., Sycamore N., Taylor R., Tree L., Thomas D. W., Thorpe A.,

Lacey A. Tromans A.C., Vaudin M., Mall M., Willis J.M.,

Lacey A. Tromans A.C., Vaudin M., Mall M., Millis J. M.,

Lacey A., Tromans A.C., Vaudin M., Mall M., Millis S.,

Lacey A., Tromans A.C., Vaudin M., Mall M., Millish S.,

Lacey A., Tromans A.C., Vaudin M., Mall M., Mallish S.,

Lacey A., Tromans A.C., Vaudin M., Mallish J.,

Lacey A., Tromans A.C., Vaudin M., Mallish J.,

Lacey A., Tromans A.C., Vaudin M., Mallish J.,

Lacey A., Tromans A.C., Taylown M., Lace L., Thomas D.,

Lacey B., Millish B., Millish B., Millish B., Millish B., Millish B., Millish B.
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Whitehead S.L., Whittese P., Willey D.L., Williams L., Williams S.A.,
Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: May be involved in both signal transduction and cellular adhesion in the CNS.
McAndrew P.E., Frostholm A., White R.A., Rotter A., Burghes A.H.M.; "Identification and characterization of RPTP rho, a novel RPTP mu/kappa-like receptor protein tyrosine phosphatase whose expression is restricted to the central nervous system."; Brain Res. Mol. Brain Res. 56:9-21(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001).
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Besco J.A., Frostholm A., Popesco M.C., Burghes A.H.M., Rotter A.;
BMC Genomics 2:5-5(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seki N., Nomira N.; "Construction of human brain cDNA libraries
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Besco J.A., Frostholm A., Popesco M.C., Burghes A.H.M., Rotter A.
"Genomic organization and alternative splicing of the human and
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TISOIG SPECIFICITY: Expression—is restricted to the CNS.
SINILARITY: Contains 1 MAM domain.
SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
SIMILARITY: Contains 4 fibronectin type III domains.
SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                suitable for analysis of cDNA clones encoding relatively large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohara O., Nagase T., Ishikawa K.-I., Nakajima D., Ohira M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lyrosine + phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
TTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 2)
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DNA Res. 4:53-59(1997).
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                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROTEIN-TYROSINE PHOSPHATASE
PHOSPHOCYSTEINE INTERMEDIATE
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CYTOPLASMIC (POTENTIAL)
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N-LINKED (GLCNAC.
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                                                                                                                                                                                                                                                                                                                                                                        25 LNIRNSLPSSSQKMTPTKPIF----GNKMNSENVKPSHHLSFSDKYELVYPEPLESDTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                          -------MDVSDRSLRNRWNSMDSETAGPSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----IFNSSARSAMRDCLNTLQK------KEELDIIREFLELEQMTLPDDFNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  879 EMSYPRDQFQLAIRVA--DLLQHITQMKRGQGYGFKEBYEALPEGQTASWDTAKED----
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MEDLINE=91006018; PubMed=2170109;
MEDLINE=91006018; PubMed=2170109;
Structural N.Y., Strentli M., Saito H.;
Structural diversity and evolution of human receptor-like protein tyrosine phosphatases.";
EMBO J. 9:3241-3252 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Protein-tyrosine phosphatase beta precursor (BC 3.1.3.48) (R-PTP-
                   (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                    tch 21.3%; Score 477; DB 1; Length 1463; al Similarity 28.5%; Pred. No. 4.1e-25; Conservative 63; Mismatches 158; Indels 122;
(POTENTIAL)
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                                                                                 684 684 N-LINKED (GLCNAC. . .) (POTE 726 744 MIGBAID (In 1soform 2). [PITE 29 29 29 P -> A (IN REF. 3). 60 60 T -> W (IN REF. 1). 375 A -> P (IN REF. 1). 801 803 MISSING (IN REF. 1). 889 889 L -> P (IN REF. 1). 889 889 L -> P (IN REF. 1). 1463 AA; 164275 MW; BR348B3E8A4017 CRC64;
                                     N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
Missing (in isoform 2).
GLCNAC.
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                           CARBOHYD
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R GO; GO:0005883; C:integral to plasma membrane; TAS.

R GO; GO:0005883; C:integral to plasma membrane; TAS.

R GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. ..; TAS.

R GO; GO:0006796; P:protein amino acid dephosphorylation; TAS.

InterPro: IPR003987; TW III-like.

InterPro: IPR003987; TW III-like.

InterPro: IPR003987; TW Phosphatase.

InterPro: IPR003987; TYF PP.

Pfam; PF00041; fn3; i6.

R Ffam; PF00042; Typ-PP.

R Ffam; PF000702; Yphosphatase; 1.

R Ffam; PF000704; PRTPHTASE.

R PRNT; SM0066; FN3; 14.

R SMART; SM00194; TYR PHOSPHATASE 1; 1.

R PROSITE; PS50056; TYR PHOSPHATASE 2; 1.

R ROSITE; PS50055; TYR PHOSPHATASE PPP; 1.

R GIycoprotein; Transmembrane; Hydrolase; Phosphorylation; Repeat; Signal.
                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
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           tyrosine + phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: Contains I protein-tyrosine phosphatase domain.
SIMILARITY: Contains 16 fibronectin type III domains.
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EXTRACELLULAR (POTENTIAL).
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FIRRONGCTIN TYPE-III 3.
FIRRONGCTIN TYPE-III 3.
FIRRONGCTIN TYPE-III 4.
FIRRONGCTIN TYPE-III 6.
FIRRONGCTIN TYPE-III 6.
FIRRONGCTIN TYPE-III 9.
FIRRONGCTIN TYPE-III 9.
FIRRONGCTIN TYPE-III 10.
FIRRONGCTIN TYPE-III 11.
FIRRONGCTIN TYPE-III 12.
FIRRONGCTIN TYPE-III 12.
FIRRONGCTIN TYPE-III 13.
FIRRONGCTIN TYPE-III 14.
FIRRONGCTIN TYPE-III 15.
FIRRONGCTIN TYPE-III 16.
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FIBRONECTIN TYPE-III 1.
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MIM; 176882; -.
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1535 ENPNSNSKSPNIKLGAEMESLGGKRDPTQ----QKPCDGPLKPHTAYRISIRAFTQLFDE 1590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VPLGK-----NKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQMVLENNCNVIAMI 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KHLQFTKWPDHGTPASADFFIKYVR----YVRKSHITGPLLVHCSAGVGRTGVFICVDVV 375
                                                                                                                                                                                                                                                                                                                                                                                                14 DNDEREGNSGNIALRASLPSSSOKATPITKPIFGNKANSENVKP--SHHLSFSDKYELV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQIV-KKSTGKSQCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 ARSAMRDCLNTLQKKKBELDIIREFLELEQMTLPDDFNSGNTLQNRDKNRYRDILFYDSTR
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TISSUE-Skeletal muscle;
MEDLINE-94329538; PubMed-7519780;
Moeller N.P.H., Moeller K.B., Lammers R., Kharitonenkov A., Sures I.,
Ullrich A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein tyrosine phosphatase, non-receptor type 21 (BC 3.1.3.48) (Protein-tyrosine phosphatase D1).
                                                                                                                                                                                                                                                                                                                                                      92;
                                                                                                                                                                                                                                                                                                          21.3%; Score 477; DB 1; Length 1997; 30.1%; Pred. No. 6.2e-25; ive 67; Mismatches 166; Indels 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 ----YPEPLESDIDBTVWDVSDRSLRNRWNSMDSBTAGPSKTVSPVLSG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOQLDSKDSVDIYGAVHDLRLHRVHMVQTECQYVYLHQCVRDVLR 1965
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Last annotation update)
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01-NOV-1997 (Rel. 35, Last seq
10-OCT-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                                                      224267
                                                                                                                                                                                                                                                                                                                                                      Matches 140; Conservative
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1157 YTEVYRVLIQFLKS 1170
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                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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Q64455;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          808 RARRDSL-----KKRPVSDLLSGKKNIVEGLPPLGGAKKTRVDAKKIGPLKLAALNGLS 861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                922 AERNREGDVE PYDDARVELVPTKENNTGYINASHIKVSVSGIEWDYIATQGPLQNTCQDP
"Src kinase associates with a member of a distinct subfamily of protean-tyrosine phosphatases containing an ezrin-like domain."; Proc. Natl. Acad. Sci. U.S.A. 91:7477-7481(1994).
-!- CATALYIIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                       tyrosine + phosphate. Similarins 1 FERM domain. Similarity: Contains 1 FERM domain. SIMILARITY: Belongs to the protein-tyrosine phosphatase family. Non-receptor class subfamily.
                                                                                                                                                                                                                                                                                                                                                                                          R MIM; 603271; C:cytoskeleton; TAS.

GO; GO:0004725; F:protein tyrosine phosphatase activity; TAS.

GO; GO:0004725; F:protein tyrosine phosphatase activity; TAS.

GO; GO:0006470; F:protein amino acid dephosphorylation; TAS.

R InterPro; IPR00029; Band 4.1.

R InterPro; IPR000342; TYF phosphatase.

R InterPro; IPR000342; TYF pp.

R Pfam; PP00373; Band 41; 1.

R Pfam; PP00373; Band 41; 1.

R PRINTS; PR00935; BAND41.

R PRINTS; PR00935; BAND41.

R SWART; SM00194; PTPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN-TYROSINE PHOSPHATASE.
PHOSPHOCYSTBINE INTERMEDIATE
(BY SIMILARITY).
POLY-PRO.
POLY-PRO.
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SMART; SMOULS4; PTPC; 1.

PROSITE; PS00660; PERM 1; 1.

RPOSITE; PS00367; FERM 2; 1.

R PROSITE; PS0367; FERM 3; 1.

R PROSITE; PS03085; TYR PHOSPHATASE 1; 1.

R PROSITE; PS50056; TYR PHOSPHATASE PPP; 1.

R PROSITE; PS50056; TYR PHOSPHATASE 2; 1.
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                                                                                                                                                                                                                                                                                                          EMBL; X79510; CAA56042.1; -. PIR; I38140; I38140.
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Best Local Similarity 30.2
Matches 131; Conservative
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MIM; 603271; -.
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                                1097 PQSPNPPLLVHCSAGVGRIGVVILSEIMIACLEHNEVLDIPRVLDMLRQQRWMLVQTLCQ 1156
---TVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYV----RKSHITG- 353
                                                                                                  ----PLLVHCSAGVGRTGVPICVDVVPSAIBKNYSFDIMNIVTQMRKQRCGMIQTKEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein-tyrosine phosphatase eta precursor (EG 3.1.3.48) (R-PTP-eta)
(HPTP beta-like tyrosine phosphatase) (Protein-tyrosine phosphatase
receptor type J) (Susceptibility to colon cancer-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tyrosine + phosphate.
-- SUBCELLULAR LOCATION: Type I membrane protein.
-- TISSUE SPECIPICITY: Expressed in every tissue examined.
-- SIMILARITY: Contains I protein-tyrosine phosphatase domain.
-- SIMILARITY: Contains 6 fibronectin type III domains.
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MEDLINE-96140699; PubMed-8549806;
Kuramochi S., Matsuda S., Matsuda Y., Saitoh T., Ohsugi M.
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LOSINE (PCTE) (POTE) TYPE-1 TY	CHUNAC CONTROL CONTR	21.2%; Score 475; DB 1; Length ; Conservative 63; Mismatches 115; Indel SKDTETSVSEKELTQLAQIRPLIFNSSARSAWRDCLATLQKKEELD : :	MILPDDENSGNTLQNRDÄGRRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEE
	NITAKITY) SIMILAKITY) 1. LINNED (G. 1.0. N. LINNE	21.2%; Score 4 34.0%; Pred. N iive 63; Mism UTQLAQIRPLIFNSS	MTLPDDFNSGNTLQNRDXGNRYRDILPYDSTRVPLG- :::
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June 16, 2004, 13:17:25; Search time 46 Seconds (without alignments) 2921.973 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		O55082 mus musculu	Q9y406 homo sapien	Q64512 mus musculu	Q28006 bos taurus	Q8n4s3 homo sapien	044328 hirudo medi	Q9iai8 xenopus lae	Q9wu22 mus musculu	O91118 mus musculu	Q9iba0 potamotrygo	090yj4 brachydanio	Q9iba2 potamotrygo	Ogum81 homo sapien	090947 qallus qall	Q8r169 mus musculu	Q8vbv0 mus musculu
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488.5 486	484 484	483	483	483	483	480	479.5	479	478.5	478.5	478	477.5	476.5	476.5	476	476	475.5	475	475	475	474.5	474.5	473.5	473.5	473.5	473.5
17	19	21	22	23	24	25	26	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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SEQUENCE FROM N.A.

STRAIN=C57BL/61; TISSUE=Testis;

X MEDINE=2234683; PubMed=1246851;

X The FANTOM Consortium,

the RIKEN Genome Exploration Research Group Phase I & II Team;

Analysis of the mouse transcriptome based on functional annotation of 60,700 full-length cDNAs.";

IN alture 420:563-573 (2002).

R WHEL; MAC029493; BAC26476.1; -.

R WHEL; AK029493; BAC26476.1; -.

R MGD; MGI:1196295; Ptpn20.

R GO; GO:0006470; F:prenylated protein tyrosine phosphatase act. ..; IEA.

GO; GO:0006470; F:prenylated protein tyrosine phosphatase act. ..; IEA.

R GO; GO:0006470; F:prenylated brotein tyrosine phosphatase.

InterPro; IPR000387; TYR_phosphatase.
                                                                                                                                        Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                      TISSUB-Testis,
MEDLINE=98070510; PubMed=9407093;
MEDLINE=98070510; PubMed=9407093;
Ohsugi M., Kuramochi S., Marsuda S., Yamamoto T.,
Molecular cloning and characterization of a novel cytoplasmic protein-tyrosine phosphatase that is specifically expressed in spermatocytes.";
J. Biol. Chem. 272:33092-33099(1997).
                                                         ollum-1998 (TrEMBirel. 06, Created) 01-JUN-1998 (TrEMBirel. 06, Last sequence update) 01-JUN-2003 (TrEMBirel. 24, Last annotation update) Protein-tyrosine-phosphatase (EC 3.1.3.48).
                                    426 AA.
                                    PRT;
                                    PRELIMINARY;
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                                    055082
RESULT 1
O55082
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SFSDKYELVYPEPLESDIDETV#DVSDRSLRNRRNSMDSSIAGPSKTVSPVLSGSSRLSK 120
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                                                                                                                                                                                          100.0%; Score 2241; DB 11; Length 426; 100.0%; Pred. No. 5.4e-167; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                      2B35FB13379502F4 CRC64;
InterPro; IPR000242; Tyr PP.
Pfam; PF00102; Y_bhosphatase; 1.
PRINTS; PR00700; PRTYPHPHTASE.
SMART; SMO194; PTPc; 1.
PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE 2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE 2; 1.
                                                                                                                                                        426 AA; 49118 MW;
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Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. s S Alsoure Minkey, Mirkner U., Mewes H.W., Gassenhuber J., Wiemann S. Ansorge W., Wirkner U., Mewes H.W., Gassenhuber J., Wiemann S. Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, ALGS0040; CA343248.1; -.

PIR: T08716; T08116.

PIR: T08716; T08116.

GO: GO:001247; Espretein tyrosine phosphatase activity; IEA.

GO: GO:0006470; F:protein amino acid dephosphorylation; IEA.

InterPro; IPR000242; TYR_PDP. 094406 PRELIMINARY; PRT; 398 AA. 097406; O97406; O1-NOV-1999 (TEMBLrel. 12, Created) O1-NOV-1999 (TEMBLrel. 12, Last sequence update) O1-UJVA-2003 (TEMBLrel. 24, Last annotation update) Bypothetical protein (Fragment) SEQUENCE FROM N.A.

MEDLINE-95145716; PubMed=7843407; Chida D., Kume T., Mukouyama Y., Tabata S., Nomura N., Thomas

3 159 218 190 99 18 PQAQVPENKVNSEKVKLSLRNFPHNDYEDVFEEPSESGSDPSMWTARGPFRRDRWSSEDE 77 PTKPIFGNKMNSENVKPSHHLSPSDKYELVYPEPLESDTDETVWDVSDRSLRNRMNSMDS ETAGPSKTVSPVLSGSSRLSKDTETSVSEKELTQLAQIRPLIFNSSARSAMRDCLNTLQK K-BELDIIREFLELEQMILPDDFNSGNTLQWRDKWRYRDILPYDSTRVPLGKNKDYINAS LKEPLEFEHFSVFLETFHVTQYPTVRVFQIVKKSTGKSQCVKHLQPTKWPDHGTPASADP FIKYVRYVRKSHITGPLLVHCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQR Q64512 PRELIMINARY; PRT; 2460 AA.

Q64512; Q62135; Q61494; Q64499;
01-NOV-1996 (TEMBLEI. 01, Created)
01-NOV-1996 (TEMBLEI. 24, Last sequence update)
01-UN-2003 (TEMBLEI. 24, Last annotation update)
Protein-tyrosine phosphatase, NONRECEPTOR-type, 13 (EC 3.1.3.48)
(Protein-tyrosine phosphatase RIP) (Phosphoprotein phosphatase RIP) (Phosphoprotein phosphatase)
(Protein-tyrosine-phosphatase) (Prosphotyrosine phosphatase) Hendriks W., Schepens J., Baechner D., Rijss J., Zeeuwen P., Zechner U., Hameister H., Wieringa B., "Molecular cloning of a mouse epithelial protein-tyrosine phosphatase with similarities to submembranous proteins."; Gaps Mus musculus (Mouse). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. ô Length 398; 58.5%; Score 1310; DB 4; Length 3 65.4%; Pred. No. 3.3e-94; ive 48; Mismatches 78; Indels 398 AA; 45690 MW; 857AAD03747870A2 PRINTS; PRO0700; PRITYPHPHTASE.

PRART; SMO10194; PTPC: 1.

PROSITE; PS00183; TYR PHOSPHATASE 1; 1.

PROSITE; PS50056; TYR PHOSPHATASE 2; 1.

PROSITE; PS50055; TYR PHOSPHATASE PTP; 1.

Hypochetical protein Hydrolase. 399 CGMIQTKEQYQFCYBIVLBVLQNLLAL 425 SGWQTKEQYHFCYDIVLEVLRKLLTL 397 SEQUENCE FROM N.A. STRAIN-C57BL/6; TISSUE-SKIN; MEDLINE-96340953; PubMed-8749712; Cell. Biochem. 59:418-430(1995) al Similarity 65.4 253; Conservative SEQUENCE FROM N.A. NCBI_TaxID=10090; PTPN13 OR PTP14. 160 279 251 311 40 100 78 SEQUENCE 339 Query Match 371 Local Best Loca Matches RESULT 3 064512 REER REER S 셤 셤 g δ ò ઠે ď ò ద ò ò g à

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RESULT 4
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STRAIN=CB.17 SCID; TISSUE=THYMUS;
MEDLINE=94554845; PubMed=8074693;
Sawada M., Ogata M., Fulino Y., Hulino Y.,
"cDNA cloning of a novel protein tyrosine phosphatase with homology to cytoskeletal protein 4.1 and its expression in T-lineage cells.";
Biochem. Biophys. Res. Commun. 203:479-484(1994).
                  "Characterization of a protein tyrosine phosphatase (RIP) expressed at a very early stage of differentiation in both mouse erythroleukemia and embryonal carcinoma ells."; FEBS Lett. 358:233-239(1995).
                                                                                                                                                                                                                                                                                         SEQUENCE OF 2266-2372 FROM N.A.
STRATHS BALBACY,
MEDLINE=95134232; PubMed=7832766;
MEDLINE=95134232; PubMed=7832766;
MEDLINE=95134232; PubMed=7832766;
MEDLINE=95134232; PubMed=7832766;
MEDLINE=95134232; Note to the sequence of the strong of
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5 APPROXIMATE REPEATS.
DHR/GLGF REPEAT 1.
DHR/GLGF REPEAT 2.
DHR/GLGF REPEAT 3.
DHR/GLGF REPEAT 4.
Watanabe T., Oishi M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : | : : | | | : : | | 2053 TRRACSPDFLRTNGRAPEEGDTDYDGSPLPEDVPESVSSGEGKVDLASLTAASQEEKPIE 2112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2113 EDATQESRNSTTETTDGEBSSKDPPFLTNBELAALPVVRVPPSGKYTGTQLQATIRTLQG 2172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2173 LLDQGIPSKELENLQELKPLDQCLI-----GQTXENRRRRRYRYKNILPYDTTRVPLGDEG 2226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2227 GYINASFIRI FVGTQEPVYIACQGPLPTTVGDFWQWVWBQNSTVIAMMTQEVEGBKIKCQ 2286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 -----KKEELDIIREPLELEQMTLPDDFNSGNTLQNRDKNRYRDILPYDSTRVPLGKNK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 SYWPISL-KEPLEFEHPSVFLETFHVTQYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHG 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                332 TPASAD---FFIKYVRYVRKSHITGPLLVHCSAGVGRTGVFICVDVVFSAIEKNYSFDIM 388
                                                                                                                                                  233 V -> L (IN REF. 2).
306 N -> I (IN REF. 2).
312 R -> E (IN REF. 2).
313 C -> E (IN REF. 2).
321 R -> E (IN REF. 2).
322 R -> D (IN REF. 2).
323 R -> O (IN REF. 2).
324 R RHPWSKTTALLIKII -> QTPHVKDYSFVTEDNT (IN REF. 2).
325 R -> G (IN REF. 2).
326 R -> G (IN REF. 2).
327 R -> O (IN REF. 2).
328 R -> O (IN REF. 2).
329 R -> S (IN REF. 2).
3207 D -> N (IN REF. 2).
3207 D -> N (IN REF. 2).
321 R -> C (IN REF. 2).
322 R -> C (IN REF. 2).
323 R -> T (IN REF. 2).
3245 R -> QFGLOQ (IN REF. 2).
3252 R -> T (IN REF. 2).
3252 R -> C GOORGE (IN REF. 2).
3252 R -> C GOORGE (IN REF. 2 AND 3).
325250 R -> SPE29D337DESC807 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 -PSHHLSFSDKYEL-------VYPEPLESDTDETVWDVSDRSLRNRWNSM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 ------DIRTS-----VSEXELTQLAQIRPLIFNSSARSAMRDCLNTLQ-
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DHR/GLGF REPEAT 5.
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
POLY-LEU.
STA -> FTG (IN REF. 2).
HIRNSNCAPSFSN -> TSGTASRAFVSY (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.5%; Score 660; DB 11; Length 2460; 32.6%; Pred. No. 2.8e-42; ive 74; Mismatches 154; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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01-JUN-2003 (
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2100 DTYCDGSPLPEDPTESTWANGCERHCERKGEKSESLIQKSEEKKTEDDEITWGSDELPIET 2159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         346 VRXSHITGPLLVHCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVFQMRKQRCGMIQTK 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 REFLELEGWILPDDFNSGNILQNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHE 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
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                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Marmalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Vega Q.C., Walton K.M., Dixon J.E.;

"Tyrosine Phosphatases and the Cytoskeleton.";

Submitted (FEBL-1995) to the EMBL/GenBank/DDBJ databases.

BMBL; U20807; AAA73516.1;

GO; GO:00018856; C:Cytoskeleton; IBA.

GO; GO:0001722; F:protein tyrosine phosphatase activity; IBA.

GO; GO:0001724; F:protein amino acid dephosphorylation; IEA.

InterPro: IPR001299; Band_4.1.

InterPro: IPR001299; Band_4.1.

InterPro: IPR001391; TYR_phosphatase.

InterPro: IPR001391; TYR_phosphatase.

InterPro: IPR001391; Band_4.1:

InterPro: IPR001395; Band_4.1:

Pfam: PF001373; Band_4.1:

Pfam: PF001373; Band_4.1:

PRINTS; PR001905; BAND41.

PRINTS; PR001905; BAND41.

PRINTS; PR001906; PETYPHPHTASE.

SMART; SM00228; PDZ; 5.

PROSITE; PS00660; FERM 1; FALSE_NEG.

PROSITE; PS00661; FERM 2; FALSE_NEG.

PROSITE; PS00661; FERM 2; FALSE_NEG.

PROSITE; PS00661; FERM 1; FALSE_NEG.

PROSITE; PS006661; FERM 1; FALSE_NEG.

PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 PSSSQXMTPTKPIFGNKANSENVKPSHHLSFSDKYBLVYPE-----
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                                                                                                                                                Sovidae, Bovinae, Bos.
Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                         NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 ONRDKNRYRDILPYDSTRVPLGKNKDYINASYI-----RIVNHEEEYFYIATQGPLPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 IAYVSREMLVINTQTGEEHTVTHLQYVAWPDHGVPDDSSDFLEFVNYVRSLRVDSBPVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 HCSAGVGRIGVFICVDVVFSAIBKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYBIVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299 QYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHI-TGPLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Renal adenocarcinoma;

A Straubberg R.;

Straubberg R.;

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, BCO33716.1; -.

GO; GO:0005483; F:binding; IEA.

GO; GO:0005483; F:binding; IEA.

GO; GO:0006470; P:protein tyrosine phosphatase activity; IEA.

GO; GO:0006470; P:protein tyrosine phosphorylation; IEA.

GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.

GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.

R GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.

R InterPro; IPR001993; Mitcoch carrier.

R InterPro; IPR001093; TYR_PP.

R PRIMTS; FR00700; PRTYPHPHTASE.

R PRIMTS; FR00700; PRTYPHPHTASE.

R PRIMTS; FR00700; PRTYPHPHTASE.

R PROSITE; SS00014; PTPC. motif; 1.

R PROSITE; PS00033; TYR_PHOSPHATASE_1; 1.

R PROSITE; PS00033; TYR_PHOSPHATASE_2; 1.

R PROSITE; PS00055; TYR_PHOSPHATASE_2; 1.

R PROSITE; PS00055; TYR_PHOSPHATASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           292 AA; 33121 MW; 54BB38BDD41D1BD7 CRC64;
                                                                                                                                                                                                                                                                QBN483;
01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.3%; Score 500; DB 4;
42.0%; Pred. No. 5.1e-31;
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                                                                                                                                                                                                                                   292 AA
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                                    2454 DQYIFCYQVILYVLTRLQA 2472
406 EQYOPCYEIVLEVLONLLA 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 42.0%
Matches 102; Conservative
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                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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SEQUENCE
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O44328
ID O4433
AC O4433
                                                                                                                                                                  RESULT 5
Q8N4S3
                                                                                                                                                                                                                                                                        SO DE RESERVA DE RESERVA DE PERTORES DE PE
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Q9WU22;
01-NOV-1999 (TrEMBLrel, 12,
01-NOV-1999 (TrEMBLrel, 12,
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Matches 110; Conservative
                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                              MEDLINE-9819536; PubMed=9526016; Macagno E.R.; Gershon T.R., Baker M.W., Nitabach M., Wu P., Macagno E.R.; Gershon T.R., Baker M.W., Nitabach M., Wu P., Macagno E.R.; Two receptor tyrosine phosphatases of the LAR family are expressed in the developing leech by specific central neurons as well as select peripheral neurons, muscles, and other cells."; J. Neurosci. 18:291-3002(1998).

EMBL; AF017083; AAB91460.1; -. BMRL; AB9170938; T30938.

HSSP; P28827; TRPM.
GO; GO:0016737; F:protein tyrosine phosphatase activity; IEA.
GO; GO:00064725; F:protein amino acid dephosphorylation; IEA.
InterPro; IPR003962; PNIII subd.
InterPro; IPR003961; FW III ...
InterPro; IPR003961; FW III ...
InterPro; IPR003963; FW Plix-like.
InterPro; IPR003963; TYR phosphatase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1758 -----SAHMQKLLEP-LITITGGSGHSTTTTGTEAEFXXL------SGKTSL----- 1797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----SSFASANLSCNKQKNRLVNVLPYETTRVCLQPIRGVDG 1835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 MDSETAGPSKTVSPVLSGSSRLSKDTETSVSEKELTQLAQIRPLIFNSSARSAMRDCLNT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 LQKKEELDIIREFLELBOMTLPDDFNSGNTLQNRDKNRYRDILPYDSTRVPLG----KM 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 KDYINASYIRIVNHEBEYFYIATQGPLPETIEDFWQMVLENNCNVIAWITREIECGVIKC 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSYWPISLKEPLEFEHFSVF-LETFHVTQYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDH 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              331 GTPASADFFIKYVRYVRKSH----ITGPLLVHCSAGVGRTGVFICVDVVFSAIBKNYSFD 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 KMIPIKPIFGNAMSENVKPSHHISFSDKYELVYPEPLESDIDETVWDVSDRSLRNRWNS
                                                                                                                                                                   Hirudo medicinalis (Medicinal leech).
Bh&aryota, Metazoa, Annelida, Clitellata, Hirudinida, Hirudinea,
Aryochobdellida, Hirudiniformes, Hirudinidae, Hirudo.
NCBI_TaxID=6421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5; Length 2051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.2%; Score 497.5; DB 5; Length ilarity 31.8%; Pred. No. i.1e-29; Conservative 69; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PSSO835; IG'LIKE; 3.
PROSITE; PSO0383; TYR PHOSPHATASE 1; 2.
PROSITE; PSSO056; TYR PHOSPHATASE 2; 2.
PROSITE; PSSO055; TYR PHOSPHATASE PP; 2.
HYGYCLASE; Immunoglobulin domain; Repeat.
SEQUENCE 2051 AA; 229604 MW; D60FBA032F659B00 CRC64;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00041; fn3; 8.
Pfam; PF00047; ig; 3.
Pfam; PF00102; x phosphatase; 2.
PRINTS; PF00104; PNTYPEIII.
PRINTS; PR0010019; PRTYPHPHTASE.
                                                                                                         Receptor tyrosine phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00408; IGC2; 3
SMART; SM00194; PTPC; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00060; FN3; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 125; Conserv
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Matches
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501 RTVRQFQFTDWPEQGVPKSGEGFIDFIGQVHKTKEQFGQDGPISVHCSAGVGRTGVFITL 560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    444 VALTKIREMGREKCHQYMP--AERSARYQYFVVDPMAEYNMPQYI-IREFKVTDARDGQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 QCVKHLQFTKWPDHGTPASADPFIKYYRKSH----ITGPLLVHCSAGVGRIGVPICV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 RDCLATLOXKEELDIIREF--LELEOMTLPDD-----FNSGNTLQNRDXNRYRDILPYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             326 RNLYTYIQNEAQIDVGEHVIGMELEFKRLANSKAHTSRFISANLPCNKFKNRLVNIMPYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 AMITREIECGVIKCYSYWPISLKEPLEFEHFSVF-LETFHVTQYFTVRVFQIVKKSTGKS
                                                                                                                                                                                                                                                                      OJIAI8;

OJ-OCT-2000 (TREMBLrel. 15, Created)

O1-OCT-2000 (TREMBLrel. 15, Last sequence update)

O1-OTS-2003 (TREMBLrel. 24, Last annotation update)

Receptor protein tyrosine phosphatase CRYP-alpha (Fragment).

Receptor protein tyrosine phosphatase CRYP-alpha (Fragment).

Receptor protein tyrosine phosphatase CRYP-alpha (Fragment).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;

Amphibia; Batrachia, Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20193505; PubMed=10727868;
Johnson K.G., Holt C.E.;
"Expression of CRYP-alpha, LAR, PTP-delta, and PTP-rho in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0016787; Fivydrolase activity; IEA.
GO; GO:0004725; Fivydrolase activity; IEA.
GO; GO:0004725; Fivotein tyrosine phosphatase activity; IEA.
GO; GO:000470; Protein amino acid dephosphorylation; IEA.
InterPro; IPR000242; TX phosphatase.
InterPro; IPR000242; TY PP.
Pfam; PR00102; V_phosphatase; 2.
PRINTS; PR00100; PRTYPHPHTASE.
SMART; SM00194; PTPc; 2.
PROSITE; PS500383; TYR PHOSPHATASE 1; 2.
PROSITE; PS50055; TYR PHOSPHATASE 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373 DVVPSAIBKNYSPDIMNIVTOMRKORCGMIQTKRQYQFCYBIVLBVL 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 496.5; DB 13; Length
; Pred. No. 2.6e-30;
53; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        615 AA; 70728 MW; 42593554887858AC CRC64;
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Last sequence update)
                                     2011 VFQTVNVLRTQRPGMVQTBEQYAFCYRAALEYL 2043
387 IMNIVIQMRKQRCGMIQTKBQYQFCYBIVLEVL 419
                                                                                                                                                                                                                                           615 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              developing xenopus visual system.", Mech. Dev. 92:291-294 (2000).
EMBL, AF199450; AAF43607.1; -.
                                                                                                                                                                                                                                           PRT;
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us-09-095-478a-5.rspt

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348 --KSHITGPLLVHCSAGVGRIGVFICVDVVPSALEKNYSPDIMNIVTOMRKORCGMIQTK 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          395 NSL-SCSQSFIQASPVSSNLSIPGSDIMRADYI-PSHRHS----TIIVPSYRPTPDY3T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 VW------DVSDRSLRNRWNSMDSETAGPSKTVSPVLSGSSRLSKDTET-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 -----SVSEKELT-QLAQIRPLIF------NSSARSAMRDCLNTLOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 NSIPSSSQXMTPTKPIFGNK------MNSENVKPSHHLSFSDKYELVYPEPLESDTDET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adyana K., Mateuda T., Aoki N.;
"Characterization of newly identified four isoforms for a putative "Characterization of newly identified four isoforms for a putative cytosolic protein tyrosine phosphatase PTP36.";
Biochm. Biophys. Res. Commun. 266:523-531(1999).
EMBL; AF170903; AAF27549.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
VCII_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96;
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MGD; MGI:102467; Ptpn14.
MGD; MGI:102467; Ptpn14.
GO; GO:0005856; C:cytoskeleton; IEA.
GO; GO:00164725; P:protein tyrosine phosphatase activity; IEA.
GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000242; TXR phosphatase.
InterPro; IPR000242; TXR phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.0%; Score 494; DB 11; Length 84
31.1%; Pred. No. 6.4e-30;
ive 72; Mismatches 156; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       849 AA; 97656 MW; 4945441F3F00B4EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00660; FERM 1; 1.
PROSITE; PS00661; FERM 2; 1.
PROSITE; PS00057; FERM 2; 1.
PROSITE; PS00383; TYR PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR PHOSPHATASE 2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20068798; PubMed=10600535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PP00373; Band 41; 1.
Pfam; PF00102; Y phosphatase; 1.
PRINYS; PR00935; BAND41.
PRINYS; PR00700; PRIVPHPHTASE.
SMART; SM00295; B41; 1.
SMART; SM00194; PTPC; 1.
                                                                                                                                                                                                                 406 EQYOFCYBIVLEVIO 420
                                                                                                                                                                                                                                                 ||:| | :| :
899 SQYRFVCEAILKVYE 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-JUN-2003 (TrEMBLrel. 24, PTP36-B isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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Q9JLJ8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         450 SSPSQETPEDGQPPALPPKQSKKNSWNQIHPSNSQQDLVTHTNBSFDVPSSPEKSTPNGG 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          668 GMTWSCAKLPQNISKNRYRDISPYDATRVLLKGNEDYINANYINMEIPSSSIINQ---- 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 PSKTVSPVLSGSSRLSKOTETSVSEKELTQLAQIRPLIFNSSARSAMRDCLATLQKKKEEL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         552 PADLCVPRINEGDQVVLINGRDIASHTHDQVV----LRIKASCEKHSGELVLLVRPNAVY 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 YIATQGPLPETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 FLETFHVTQ---YFTVRVFQIVKKSTGKSQCVKHLQPTKWPDHGTPASADFFIKYVRYVR 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 SSPRKVRGKTGR----DNDEREGNSGN-LNLRNS------LPSSSQKMTPTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 IFGNRAMSENVKPSHHLSFSDKYELVYPRPLESDTDETVWDVSDRSLRNRWNSMDSRTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           510 IPHDNLVLIKÆKPDENGRFGFNVKGGYDQYMPVIVSRVA------PGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 ------QNRDKARYRDILPYDSTRVPLGKNKDYINASYIR-----IVAHEEBYF
                                                                                                                                                                                                                                                                                             MEDIINE=20510023; PubMed=11054567;
Park K.W., Lee E.J., Lee S.H., Lee J.E., Choi E.Y., Kim B.J.,
Hwang R., Park K.A., Baik J.H.;
"Molecular cloning and characterization of a protein tyrosine
phosphatase enriched in testis, a putative murine homologue of human
PTPMEG.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 22.1%; Score 495.5; DB 11; Length 926;
Best Local Similarity 27.5%; Pred. No. 5.5e-30;
Matches 136; Conservative 76; Mismatches 176; Indels 107; Gaps
                                                                                                          Bukaryota; Netazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               926 AA; 105713 MW; A344DAD4FF7E2AE2 CRC64;
            01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Testis-enriched protein tyrosine phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00660; PERM 1; 1.
PROSITE; PS00661; PERM 2; 1.
PROSITE; PS50057; PERM 3; 1.
PROSITE; PS50106; PDZ, 1.
PROSITE; PS00108; TYR, PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR, PHOSPHATASE 2; 1.
PROSITE; PS50056; TYR_PHOSPHATASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00295; B41; 1
SMART; SM00228; PDZ; 1
SMART; SM00194; PTPC;
                                                                                                    musculus (Mouse)
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Gaps

374

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"Expression of receptor protein-tyrosine phosphatase alpha, sigma and LAR during development of the zebrafish embryo.";

Lan during development of the zebrafish embryo.";

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ31886; CAC44759.1;

ZPIN; ZDB-GENE-020107-3; ptprs.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.

GO; GO:0004725; F:protein amino acid dephosphorylation; IEA.

InterPro; IPR000397; FY III-like.

RIMETPRO; IPR000397; FY PP.

RIMETPRO; IPR000342; TYR Phosphatase.

RIMTS; PR00700; PRTYPHHHASE.

SMART; SM00104; YDHOSPHATASE.

RRART; SM00194; PTPC; 2.

RROSITE; PS50056; TYR PHOSPHATASE.

RROSITE; PS50056; TYR PHOSPHATASE.

RROSITE; PS50055; TYR PHOSPHATASE.

RROSITE; PS50055; TYR PHOSPHATASE.

RROSITE; PS50055; TYR PHOSPHATASE.

RROSITE; PS50055; TYR PHOSPHATASE.
                                                                                                                                                           375 GFIDFIGQVHKTKEQFGQDGPISVHCSAGVGRTGVFITLSIVLERÆRYEGVVDIPQTVYM 434
279 LKEPLEFEHFSVF-LETFHVTQYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASAD 337
                                                                                                                        338 PFIKYVRYVRKSH----ITGPLLVHCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQ 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315 KSQCVRHLQPTKWPDHGTPASADPPIKYVRXVRKSH----ITGPLLVHCSAGVGRTGVFI 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     741 QSRTVRQFQFTDWPEQGVPKSGEGFIDFIGQVHKTKEQFGQDGFISVHCSAGVGRTGVFI 800
                                  201 YDSTRVPLG-----KNKDYINASYIRIVNHEBEYFYIATQGPLPETIEDFWQMVLENNCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           256 VIAMITREIECGVIKCYSYMPISLKEPLEFEHFSVP-LETFHVTQYFTVRVFQIVKKSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 AMRDCLNTLOKKGELDIIREF--LELEQMTLPDD-----FNSGNTLQNRDKNRYRDILP
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
Receptor protein-tyrosine phosphatase sigma (Fragment).
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Caniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBL TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.0%; Score 493.5; DB 13; Length 857; 38.1%; Pred. No. 7.1e-30; tive 54; Mismatches 102; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371 CVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVL 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. van der Sar A., Betist M., de Fockert J., Overvoorde J., den Hertog J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     857 AA
                                                                                                                                                                                                                                                                                                        435 LRTQRPAMVQTEDEYQFCYQAALEYL
                                                                                                                                                                                                                                                 394 MRKQRCGMIQTKEQYQPCYBIVLEVL
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es 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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Matches
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                        KSELDIIRBFLELEQMTLPDD----FNSGNTLQNRDKNRYRDILPYDSTRVPL---GK 210
                                                                                                                                                       270
                                                                                                                                                                                      323
                                                                                                                                                                                                                                                                                                                                           681 SHRYWP-----KLGSKHSSATYGKFKVTTKFRTDSGCYATTGLKVKHILSGQERTVWHLQ 735
                                                                                                                                                                                                                                                                                                                                                                                                                324 FIXMPDHGTPASADFFIKY-----VRYVRKSHITG------PLLVHCSAGVGRTGVFIC 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       736 YIDWPHHGCPEDVQGFLSYLEBIQSVRRHTNSVLEGIRTRHPPIVVHCSAGVGRTGVVIL 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 LELECATIPDD-----FNSGNTLQNRDKNRYRDILPYDSTRVPLG----KNKDYINAS 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 MELEFKRLANSKAHTSRFISANLPCNKFKONRLVNIMPYETTRVCLOPIRGVEGSDYINAS 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 YIRIVNHEEEYFYIATQGPLPETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPIS 278
                                                              NKDY INASYIRIVNHEEEYFYIATQGPLPETIEDFWQMVLENNCNVIAMITREIECGVIK
                                                                                                                                                                                                                                                                             271 CYSYWPISLKEPLEFEHFSVFLETFHVTQYF-----TVRVFQIVKKSTGKSQCVKHLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20219325; PubMed=10754074;
Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;
"Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
divergence of tissue-specific isoform genes in the early evolution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potamotrygon motoro (South American freshwater stingray).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes,
Elasmobranchii, Squalea, Hypnosqualea, Pristiorajea, Batoidea,
Myliobatiformes; Myliobatoidei, Potamotrygonidae, Potamotrygon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372 VDVVPSALEKNYSPDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQN 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  396 SELMIYCLEHNEXVEVPTMLRFLREQRMFMIQTIAQYKFVYQVLVQFLQN 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.0%; Score 493.5; DB 13; Length 468; 40.2%; Pred. No. 3.1e-30; Live 48; Mismatches 90; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOSTIE: F10.016.787; F10.016.78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               468
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J. Mol. Bvol. S0:302-311(2000).
EMBL; AB033586; BAA95193.1; --
HSSP; P18052; IXPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 40.2<sup>3</sup>
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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MEDLINE=20219325; PubMed=10754074;
MEDLINE=20219325; PubMed=10754074;
MEDLINE=20219325; PubMed=10754074;
MEDLINE=20219325; PubMed=10754074;
MEDLINE=20219325; PubMed=10754074;
MINO-KONGANGATE K. Suga H., Katoh K. amphioxus, hagfish, and ray:
divergence of tissue-specific isoform genes in the early evolution of vertebrates.*;
J. Mol. Bvol. 50:302-311(2000).
R BMBL; AB033584; BAA95191.1; -.
HSSP; P18052; HYFO.
GO; GO:00167787; P:protein tyrosine phosphatase activity; IEA.
GO; GO:006470; P:protein tyrosine phosphorylation; IEA.
InterPro: IPR000242; TYR phosphatase.
A InterPro: IPR000242; TYR phosphatase.
Brim; PR00100; PRTYPHPHIASE.
R FRINTS; SM00194; PTPC; Z.
R FRINTS; SM00194; PTPC; Z.
R FRINTS; PR001005; TYR PHOSPHATASE_1; Z.
R FROSITE; PS50056; TYR PHOSPHATASE_2; Z.
R PROSITE; PS50055; TYR PHOSPHATASE_PTP; Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 FID--GYRQQKAYIATQGPLAETTEDFWRMLWEHNSTIVVWLTKLREMGREKCHQYWP-- 315
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01-0CT-2000 (TYEMBLEEL. 15, Last sequence update)
01-0TG-2003 (TYEMBLEEL. 24, Last annotation update)
01-0TG-2003 (TYEMBLEEL. 24, Last annotation update)
RyPTREAD protein (Fragment).
RYPTREAD.
RYPTRE
801 ILSIVLERMRYEGVVDIFQTVKMLRTQRPANVQTEDEYQFCYQAALEYL 849
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                                                                                                                                                                              PRT; 1502 AA.
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01-MAY-2000 (TrEMBLrel. 13, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279 IKEPLEFEHFSVF-LETFHVTQYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 LELEQMILPDD-----FNSGNTLQNRDKNRYRDILPYDSTRVPLG-----KNKDYINAS
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                                                                                                                                                SEQUENCE FROM N.A.
Budo N., Rutledge S.J., Opas B.E., Vogel R., Rodan G.A., Schmidt A.,
"Hunan protein tyrosine phosphatase-sigma: Alternative splicing and
inhibition by biophosphanates.";
                                                                           Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 1502;
                                                                                                                                                                                                                                                           GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0004725; F:procein tyrosine phosphatase activity; IEA.
GO; GO:0004725; F:procein tyrosine phosphatase activity; IEA.
GO; GO:0006470; P:procein tyrosine phosphorylation; IEA.
InterPro; IPR003962; FnIII subd.
InterPro; IPR003961; FN III.like.
InterPro; IPR003981; FN III.like.
InterPro; IPR003891; Ig-21.
InterPro; IPR00387; TYR_phosphatase.
InterPro; IPR00387; TYR_phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.9%; Score 490.5; DB 4; Length 40.2%; Pred. No. 2.6e-29; ive 47; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168788 MW; AD6705AFEB0F3CPD CRC64;
      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q90947;
01-NNV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS00383; TYR PHOSPHATASE 1; 2.
PROSITE; PS50056; TYR PHOSPHATASE 2; 2.
PROSITE; PS50055; TYR PHOSPHATASE PTP: 2.
Hydrolase; Immunoglobulin domain; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     394 MRKQRCGMIQTKBQYQFCYBIVLEVL 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PP00041; fn3; 4.
Pfam; PP00047; iq; 3.
Pfam; PP00102; Y phosphatase; 2.
PRINTS; PR00104; FNTYPEIII.
PRINTS; PR00700; PRTYPHPHTASE.
                                                                                                                                                                                                              J. Bone Miner. Res. 0:0-0(1995).
EMBL; U41725; AAD09360.1; -.
HSSP; P18052; 1YPO.
01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
                    01-OCT-2003 (TrEMBLrel. 25, PTPsigma-(brain) precursor PTPSIGMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 40.2%
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00060; FN3; 4
SMART; SM00408; IGc2;
SMART; SM00194; PTPc;
                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1502 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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ID 009
AC 006
DT 001
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                                                                                                                                                                              TISSUE=Embryo;

NEDLINE=94122757; PubMed=8293038;

RWMFGY R., Leo J.M., Corbeil H.B., Charbonneau R., Jue K.,

RWMFGY R., Leo J.M., Corbeil H.B., Charbonneau R., Jue K.,

Dankort D.L., Branton P.B.;

Tisolation of chicken phosphotyrosy! phosphatase cDNA Sequences and identification of a brain-specific species related to human PTPzeta.";

Cell Mol. Biol. Res. 39:209-219(1993).

EMBL: L27625; AAA49015.1; -

EMBL: L27625; AAA49015.1; -

EMBL: L27625; Phydrollase activity; IRA.

GO: GO:0004725; F:protein tyrosine phosphotylation; IRA.

GO: GO:000470; P:protein amino acid dephosphorylation; IRA.

InterPro; IPR000242; TYR phosphatase.

InterPro; PR001024; TyR phosphatase.

PRONITE; PR00103; Phosphatase; 2.

PRNNT; SM00194; PTPC: 2.

PROSITE; PS00183; TYR PHOSPHATASE 1; 1.

PROSITE; PS00183; TYR PHOSPHATASE 2; 2.

PROSITE; PS00155; TYR PHOSPHATASE PTP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 LPHYSTFAFSSAELPPHSLSSSSGE------YGSASAAASEVLSQYTQPIYNEA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 PSHHLSFSDKYELVYPEPLESDTDETVWDVSDRSLRNRWNSWDSETAGPSKTVSPVLSGS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 SRLSKDTBTSVSEKELTQLAQIRPLIFNSSARSA-------MRDCLNTLQ----- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159 -----IREFLELEQMT--LPDDFN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 SGNTLQNRDKNRYRDILLPYDSTRVPL-----GKNKDYINASYIRIVNHEBEYFYIATQ 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 SSNHPDNKNKONRYINIVAYDHTRVKLAQLABKDGKLTDYINANYVDGYNKPKA--YIAAQ 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 TSPRVISAPPAPVFPVSDDVGAIPIKH?PKHVADLHASNGFSBEFBBIQSCTVDLGITSD 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 GPLPETIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETF 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296 HVTQYFTVRVFQI----VKKSTGK----SQCVKHLQFTKWPDHGTPASADFFIKYVRYVR 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 KS-----HITGPLLVHCSAGVGRTGVFICVDVVFSAIBKNYSFDIMNIVTQMRKQRCGMI 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 GNINIENSIPSSSOKM-----NVK 55
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Phosphotyrosyl phosphatase.
Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 SNSSHESRIGLABSLESEKKTVIPLVVVSALTPICLVILVGILIYWRKCPQTAHFYLEDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.9%; Score 490; DB 13; Length 832;
27.8%; Pred. No. 1.3e-29;
tive 81; Mismatches 158; Indels 120; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               832 AA; 93298 MW; 4A61F365B8D794F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTKROYOFCYBIVLEVL 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||:||| | :: ::| :
494 QTEEQYIFIHDALVEAI 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 27.89
Matches 138, Conservative
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase.
SEQUENCE
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655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 YIRIVNHEEEYFYIATQGPLPETIEDFWQMVLENNCNVIAMITREIBCGVIKCYSYWPIS 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               338 PRIKYVRYVRKSH----ITGPLLVHCSAGVGRTGVFICVDVVFSAIBKNYSFDIMNIVTQ 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       656 GFIDFIGGVHKTKEQFGQDGPISVHCSAGVGRTGVFITLSIVLBRMRYEGVVDIFQTVKM 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 LELEQMTLPDD-----FNSGNTLQNRDKNRYRDILPYDSTRVPLG-----KNKDYINAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279 LKEPLEFEHFSVF-LETFHVTQYFTVRVPQIVKKSTGKSQCVKHLQFTKWPDHGTPASAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.,

Strausberg R.,

Strausberg R.,

Strausberg R.,

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

RETEL; 80025445; AAHZ5145.1; -.

RETEL; 80025445; AAHZ5145.1; -.

RO; GO:0016787; F:hydrolase activity; IEA.

RO; GO:0016787; F:hydrolase activity; IEA.

RO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.

DR InterPro; IPR000347; TYR phosphatase.

DR InterPro; IPR000344; TYR PP.

DR RINTS; PR001024; YP. PP.

DR RINTS; PR00104; PPPC; 2.

RRATI; SM00134; PPPC; 2.

DR ROSITE; PS00183; TYR PHOSPHATASE 1; 2.

DR PROSITE; PS00185; TYR PHOSPHATASE 2; 2.

DR PROSITE; PS00185; TYR PHOSPHATASE 2; 2.

RW HYDOTHERICAL PROCESSIONS 1 TYR PHOSPHATASE 2.

RW HYDOTHERICAL PROCESSIONS 1 TYR PHOSPHATASE 2.

RW HYDOTHERICAL PROCESSIONS 1 TYR PHOSPHATASE 2.

RW HYDOTHERICAL PROCESSIONS 2 TYR PHOSPHATASE 2.

RW HYDOTHERICAL PROCESSIONS 3 TYR PHOSPHATASE 2.

RW HYDOTHERICAL PROCESSIONS 3 TYR PHOSPHATASE 2.

RW HYDOTHERICAL PROCESSIONS 3 TYR PHOSPHATASE 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92; Indels
                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 21.8%; Score 489.5; DB I. Best Local Similarity 40.2%; Pred. No. 1.2e-29; Matches 107; Conservative 46; Mismatches 92
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    749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               716 LRIÇRPAMVÇTEDÖYÇFCYRAALBYL 741
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-Kidney;
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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Search completed: June 16, 2004, 13:24:19 Job time : 49 secs